

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 116176

TO: Phillip Gambel

Location: 3e81 3c70

Tuesday, March 99, 2004

Art Unit: 1644 Phone: 272-0844

Serial Number: 10 / 042421

From: Jan Delaval

**Location: Biotech-Chem Library** 

**Rem 1A51** 

Phone: 272-2504

jan.delaval@uspto.gov

### Search Notes

10/042421



U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

#### **SEARCH REQUEST FORM**

Requestor's Name:			Serial Number	:		
Date:		Phone:		Ar	Unit:	
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terms that may have a	special meaning.	Give examples or	specifically as possible relevent citations, autho opy of the broadest and	ors, keyword	ls, etc., if known.	hed. Define any For sequences,
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PTO-1590 (9-90)

Title: Perfect score: Sequence:

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8, 2004, 06:08:16; Search time 21 Seconds (without alignments) 2258.211 Million cell updates/sec

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 · Contract

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RESULT 1
$13530
$13530
CD44E protein, epithelial - human
CJ5pecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: $13530
R;StamenKovic, I.; Aruffo, A.; Amiot, M.; Seed, B.
EMBO J. 10, 343-348, 1991
A;Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptide
A;Reference number: $13530; MUID:91122041; PMID:1991450
A;Accession: $1353
A;Status: preliminary
A;Molecule type: mENA
A;Residues: 1-493 <STA>
A;Cross-references: EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PID:g29801
C;Keywords: transmembrane protein
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Description
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epican - human

Database

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2: pir2:\*
3: pir3:\*
4: pir4:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Searched:
Total number
Minimum DB 84
Maximum DB 84

seq length: 0
seq length: 2000000000

of hits satisfying chosen parameters:

283366

283366 seqs, 96191526 residues

receptor CD44 revea U.; Bell,

J.I.

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RESULT 2

137369

epican - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Aug-2001
C;Accession: 137369; S24631
C;Accession: 137369; S24631
J:Invest. Dermatol. 99, 866-891, 1992
A;Title: The core protein of epican, a heparan sulfate proteoglycan on keratino A;Reference number: 137369; PMID:1281868
A;Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-699 cRES>
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lymphocyte 1
C;Species: 1
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A;Title: Genomic structure of DNA encoding the lymphocyte homing rec A;Reference number: A47195; MUID:93101687; PMID:1465456
A;Accession: A47195
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-742 <SCR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:120731, NCBIN:120737, NCBIN:120774, NCBIN:120774, NCBIN:120770, NCBIN:120772, NCBIN:120774, NCBIN:12077
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;Species: Homo sapiens (man)
;Date: 21-Sep-1993 #sequence_revision 18-
;Accession: A47195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL
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                        ALILAVCIAVNSRRRCGOKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSET
                                                      ALILAVCIAVNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSET
                                                                                                                                     SLSGDQDTFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLAL
                                                                                                                                                                                                               TGGRRDPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNR
                                                                                                                                                                                                                                                                    LOPTANPNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDV
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Pred. No. 5.1e
1; Mismatches
                                                                                                           DGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLAL
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471 660 411 600 351 540 291 480 231

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240

222 180 180 120 60

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A;Reference number: A53029; MUID:94149816; PMI
A;Accession: A53029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 67-76,'X',78-89 <SHE>
C;Genetics: GDB:CD44; MDU2; MDU3; MI
A;Gene: GDB:CD44; MDU2; MDU3; MI
A;Gene: GDB:CD44; MDU2; MDU3; MI
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
A;Introns: 35/1; 65/1; 133/1
C;Superfamily: human cell adhesion protein CD4
C;Keywords: alternative splicing; cell adhesio
C;Keywords: alternative splicing; cell adhesio
C;Keywords: lymphocyte homing rec
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R;Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datt;
Biochem, Biophys Res. Commun. 182, 569-578, 1992
A;Title: The complex CO44 transcriptional unit: alternative splicing of three internal A;Reference number: PH0859; MUID:92134271; PMID:1734871
A;Accession: PH0859
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A; Residues: 184-376 < SRO>
A; Cross-references: GB:X55938; NID:929802; PIDN:CAA39404.1
A; Cross-references: GB:X55938; NID:929802; PIDN:CAA39404.1
R; Jackson, D.G.; Buckley, J.; Bell, J.I.
J. Biol. Chem. 267, 4732-4739; 1992
A; Title: Multiple variants of the human lymphocyte homing A; Reference number: A42402; MUID:92165834; PMID:1537855
A; Accession: A42402
                                                                                                                                                                                                                                                                                      R;Shepley, M.P.; Racaniello, V.R.
J. Virol. 68, 1301-1308, 1994
A;Title: A monoclonal and the blocks policyirus attachment recognizes the A;Reference number: A53029; MUID:94149816; PMID:7508992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 217-223, 288-359
A; Note: sequence extracted f
A; Note: variant B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Brown, T.A.; Bouchard, T.; St. John, T.; J. Cell Biol. 113, 207-221, 1991
A;Title: Human keratinocytes express a new A;Reference number: A39209; MUID:91177958; A;Accession: A39209
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A; Residues: 223-357 <COO>
R; Brown, T.A.; Bouchard,
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A; Residues: 1-426 < DOU>
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A; Note: variant D
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A; Residues: 1-223, 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
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Superfamily: human cell adhesion protein CD44, splice form CD44R1 #status predicted </br>
;Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glycd; feeywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glycd; i-246/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status pre; 1-223,288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
Residues: 217-320 <JA2>
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PMID:
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CD44R5 - human
C;Species: Homo
C;Date: 02-Aug-
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A;Cross-references: GDB:120739;
A;Map position: 11pter-11p13
A;Introns: 257/1
C;Superfamily: human cell adhesi
                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_
C;Accession: I77371
C;Accession: I77371
R;Tanabe, K.K.; Nishi, T.; Saya, H.
Mol. Carcinog. 7, 212-220, 1993
A;Title: Novel variants of CD44 arising from alternative A;Reference number: 157483; MUID:93356912; PMID:8352881
                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-395 <RES>
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                                                                                                                                                                                                                                                                                               A; Cross-references:
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PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTYCFN
                                                  MDKFWWHAAWGLCLVPI
                                                                            MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL
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                                                                                                                                                                                    human cell adhesion protein CD44
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                                                                                                                                                                                                                                                                                           GB:S66400; NID:g435697; PIDN:AAB27919.1; PID:g435700
                                                                                                                                   78.1%;
79.9%;
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                                                  SLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL
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e (Ser) (covalent) #status predicted
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                 TRNLONVDMKIGV 493
                                                                                                                            HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIA
                                                     VNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE
                                                                     VNSRRRCGOKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETFDQFMTADE
                                                                                                        HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIA
                                                                                                                                                                                       SEGSTTLLEGYTSHYPHTKESRTF1PVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDODTF
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TRNLONVOMKIGV 361
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C;Genetics:
A;Gene: CD44; ECMRIII; Hermes-1 antigen
A;Gene: CD44; ECMRIII; Hermes-1 antigen
C;Superfamily: human cell adhesion protein CD44
C;Superfamily: human cell adhesion protein; glycoprotein; lipoprotein;
C;Keywords: cytoskeleton; extracellular matrix; glycoprotein; lipoprotein;
F;1-20/Domain: signal sequence #status predicted cSIG>
F;21-362/Product: lymphocyte adhesion receptor #status predicted cMAT>
F;21-362/Product: lymphocyte adhesion receptor #status predicted cMAT>
F;21-370/Domain: extracellular #status predicted cMAT>
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A;Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion 1 A;Reference number: A33935; MUID:89282830; PMID:2471974
A;Accession: A33935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lymphocyte adhesion receptor precursor - baboon
(;Species: Papio sp. (baboon)
(;Date: 18-Apr-1989 #sequence revision 18-Apr-1989 #text_change 21-Jul-2000
(;Date: 18-Apr-1989 #sequence revision 18-Apr-1989 #text_change 21-Jul-2000
(;Accession: A33935, A30901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M22452; NID:g176576; PID:g176577 C;Comment: This protein was isolated from the herpes papio
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A;Molecule type: mRNA
A;Residues: 1-362 <IDZ>
                                    ;271-290/Domain: transmembrane #status predicted <TMM>;291-362/Domain: intracellular #status predicted <CYT>;25,57,100,110,120,256/Binding site; carbohydrate (Asn)
296/Binding
    site:
palmitate (Cys)
         (covalent) #status predicted
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Query Match

65.1%;

Score 1698.5;

DB 2;

Length 362;

231

223 238

231

284 418

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lymphocyte surface antigen CD44 precursor - horse
()Species: Eguus caballus (domestic horse)
(;Date: 20-Feb-195 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
(;Accession: 146245; S24240
R.,Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis,
Immunogenetics 37, 474-477, 1993
A.,Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.
A;Reference number: 146245; MUID:93170897; PMID:8436424
A;Accession: 146245; MUID:93170897; PMID:8436424
A;Accession: 146245; MUID:93170897; PMID:8436424
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-359 cTR2>
A;Gross-references: EMBL:X66862; NID:g1059; PIDN:CAA47331.1; PID:g1060
C;Superfamily: human cell adhesion protein CD44
C;Keywords: surface antigen; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTAD 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSSERSSTSGGYIFYT-FSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPN
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                                                                                      PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTYCFN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALILAVCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSSERSSTLGGYIFYNHFSTSPPIPDEDGPWITDSTDRTPATR------
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   ASAPPEEDCTSVTDLPNAFEGPITITIVNRDGTRYTKKGEYRTNPEDINPSTPADDDVSS
                        ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 180
                                                                                                                                         MDKFWWRAAWGLCLVPLSLAQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCKAFNSTL
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                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                           59.3%; Score 1547; DB 2; 63.0%; Pred. No. 3.3e-92; Live 20; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.2%;
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7; Mismatches
                                                                                                                                                                                                              Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1e-102;
ches 17;
                                                                                                                                                                                                                                              Length 359;
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                                                                                                                                                                                                              Indels 138;
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$45305

CD44 antigen precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Species: Co-Ct-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C;Accession: $45305
R;Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.
Biochim. Biophys. Acta 1218, 112-114, 1994
A;Title: Molecular cloning of the camine CD44 antigen cDNA.
A;Reference number: $45305
A;Accession: $45305
A;Accession: $45305
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 < MIID>
A;Cross-references: EMBL; Z27115; NID:9473226; PIDN:CAA81630.1; PID:9473227
C;Superfamily: human cell adhesion protein CD44
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Matches 297; Conserv
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Best Local :
                    368
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-----AQTTHGSETSGHSTGSQEGGASTTSGPIRRPQIPEWLIILASLLALALILAVC
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TTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIAVNSRRRC
                                                                                                                                                                                                                            TSGGYIFYT-FSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNTGLVEDLD
                                                                                                                                                                                                                                                               CTSVTHLENAFDGEITITIVNRDGTRYSQKGEYRTNEEDINESNETDDDVSSGSSSERST
                                                                                                                                                                                                                                                                                                   CTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSS
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                                                                                                                                                            RTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTL
                                                                                                                                                                                                 SAGYNIFHTHLPTAYPTEDQDSSRVSSNSDHTPIT
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                                                                                        LEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTFHPSGGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.4%; Score 1470; DB 2;
61.7%; Pred. No. 2.9e-87;
ative 21; Mismatches 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 351;
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                                                          -----DSSVHPSERSH
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188

247 181

216

128 61 68

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121

427 230 367

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"ACCESSION: Ā53286; S22123
R;Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Mol. Immunol. 28, 1131-1135, 1991
A;Title: Sequence of the bovine CD44 cDNA: comparison with A;Reference number: A53286; MUID:92017904; PMID:1922105
A;Accession: A53286
A;Molecule type: mRNA
A;Residues: 1-366 < BOGS
A;COSSS-references: T.T.
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A53286.
A53286.
A53286.
Cell-surface glycoprotein CD44 precursor - bovine
C;Alternate names: CD44 protein
C;Species: Bos prinigenius taurus (cattle)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A53286; S22123
R;Bosworth, B.T.; St John, T.; Gallatin w w . uarm T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X62881; NID:g186; PIDN:CAA44675.1; PID:g187
A;Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>
F;21-367/Domain: transmembrane #status predicted <TMM>
F;25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent)
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                       QFMTADETRNLQNVDMKIGV 493
                                                                                                       ILAVCIAVNSRRRCGOKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPD
                                                                                                                                                                                                                                                          GRRDPNHSEGSTTLLEGYTSHYPHTXESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSL
                                                                                                                                                                                                                                                                                                                                 PTANPNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ASAPPGEDCTSVTDLPNAFEGPITITIVNRDGTRYTKKGEYRTNPEDINPSVVSPSSPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDI-----YPSNPTD
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                                                                                                                                                                  SGDQDTFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALAL
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 366
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Cell 61, 1303-1313, 1990
Cell 61, 1303-1313, 1990
A;Title: CD44 is the principal cell surface receptor for hyaluronate A;Reference number: A35616; MUID:90304889; PMID:1694723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Cricetinae gen. sp. (hamster)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21
C;Accession: A35616
C;Accession: A35616
R;Aruffo, A; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-362 ARUs
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-cell surface glycoprotein CD44 - hamster
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21-Jul-2000
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                       MTADETRNLONVDMKIGV
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                                                                 AVCIAVNSRRRCGQKKKLVINSGNGKVEDRKPSELNGEASKSQEMVHLVNKEPSETPDQF
                                                                                                AVCIAVNSRRRCGOKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQF
                                                                                                                                                                  D-TFHPSGGSHT-THGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLILASLLALALIL
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MTADETRNLQNVDMKIGV
                                                                                                                                   DSSMDPRGNSLTVTDGSKLTGHSSGNQDSGANTTSRPGRKPQIPEWLIVLASLLALALIL
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Pred. No. 1.6e-84;
3; Mismatches 3;
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 05-Nov-1999
C;Accession: B38745; A38745
R;Guenthert, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; HauBmann, I.;
Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to ra
A;Reference number: A38745; MUID:91191552; PMID:1707342
A;Accession: B38745
A;Accession: B38745
A;Accession: B38745

car

B38745
cell adhesion molecule CD44 precursor, long form colories: Rattus norvegicus (Norway rat)

(meta-1) -

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A;Residues: 1-503 <GUE>
A;Cross-references: GB:M61874; NI
A;Accession: A38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223,386-503 <GU2>
A;Cross-references: GB:M61875
C;Keywords: cell adhesion
                                                                                       RESULT 13
A37009
CD44 homolog membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 21-Jul-2000
C;Accession: A37009
R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; Goeddel, D.V.
J. Immunol. 143, 3390-3395, 1989
A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CAM
A;Reference number: A37009; MUID:90038499; PMID:2681416
A;Accession: A37009
A;Status: preliminary
A;Molecular type: mENA
A;Residues: 1-363 <ZHO>
A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333
C;Superfamily: human cell adhesion; glycoprotein; membrane protein
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 MDKFWWHAAWGLCLVPLSLA--QIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNS
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                                               52.5%;
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                                28;
                                             Score 1368; DB 2;
Pred. No. 1.1e-80;
                                Mismatches
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                         TADETRNLONVDMKIGV
                                                             VCIAVNSRRRCGQKKKLVINGGNGTVEDRKPSELNGEASKSQEMVHLVNKEPSETPDQCM
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                                                                                                                       -GSSRTVTHGSELAGHSSANQDSGVTTTSGPMRRPQIPEWLIILASLLALALILA
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RESULT 14
A34424
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CD44 membrane glycoprotein precursor - mouse
CJSpecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-1990 #text\_ch
C;Accession: A34424; A34907
R;Nottenburg, C.; Rees, G.; St. John, T.
R;Nottenburg, C.; Rees, G.; Re A; Molecule type: mRNĀ A; Residues: 8-195, 'G', 197-365 <WOL> A; Cross-references: GB: J05163; NID:g200334; PIDN:AAA39923.1; C; Superfamily: human cell adhesion protein CD44 C; Keywords: cell adhesion; glycoprotein; membrane protein A;Cross-references: GB:M27130; NID:g192530; PIDN:AAA37407. R;Wolffe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; J. Biol. Chem. 265, 341-347, 1990
A;Title: The cDNA sequence of mouse Pgp-1 and homology to A;Reference number: A34907; MUID:90094420; PMID:2403559 A;Accession: A34907 A; Status: preliminary A; Residues: 1-365 < NOT> A; Status: preliminary A; Molecule type: mRNA PIDN:AAA37407.1; PID:g309161 Holland, S.M.; Steinberg, A. #text\_change human CD44 cell surface are PID: g200335 distinct 01-Dec-2000 A.D.; August, from

the 'n

Local Similarity

Conservative

52.2%; Score 1361; DB 57.7%; Pred. No. 3e-80; tive 28; Mismatches

43; 2

140;

Gaps

9

60 56

Length Indels

57

NSTLPTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVXIL-TSNTSQYD MDKFWMHTAWGLCLLQLSLAHPHQQIDLNVTCRYAGVFHVEXNGRYSISRTEAADLCQAF MDKFWWHAAWGLCLVPLSLA----QIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAF

Search completed: March 8, 2004, 06:12:10 Job time : 24 secs	Qy 264 PSTSHEGLEEDKOHPTTSTLTSSNENDVTGGRRDPNHSEGSTTLLEGYT	Ch 26.8; Score 699; DB 2; Le I Similarity 69.78; Pred. No. 9.6e-38; 147; Conservative 10; Mismatches 18; 147; Conservative 10; Mismatches 18; 1	RESULT 15  S24222  CD44 protein - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: \$24222 R;Hofmann, M.; Rudy, W.; Zoeller, M.; Toelg, C.; Ponta, I Cancer Rss. 51, 5292-5297, 1991 Cancer Rss. 51, 5292-5297, 1991 A;Title: CD44 splice variants confer metastatic behavior A;Reference number: \$24222; MUID:92005448; PMID:1717145 A;Accession: \$24222 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-337 <hof> A;Cross-references: EMBL:X62739; NID:937651; PIDN:CAA446</hof>	Db 121 TYCPNASAPPEEDCTSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEBIDASNIID  Qy 176 DDVSSGSSERSSTSGGYIFYTFSTVHPIPDEDSPMITDSTDRIPATNMDSSHSTTLQFT
	TTLLEGYTSHYPHTKESRT 323	h 337; els 36; GapsPDEDSFWITD 21                 QGRTTPSPEDSSW-TD 18 RTGPLSMTTQQSNSQS 26                                       RTGPLSMTTQQSNSQS 24	change 21-Jul-2000 H.; Herrlich, P.; Guenthert, U. r in rats: homologous sequences a	

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: March 8, 2004, 06:08:16; Search time 17 Seconds (without alignments) 1510.034 Million cell updates/sec

Title: Perfect score: Sequence: PCT-US01-51014-1 2608 1 MDKFWWHAAWGLCLVPLSLA.....QFMTADETRNLQNVDMKIGV 493

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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# ALIGNMENTS

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  RC TISSUE-Lymphoblast;  RX MEDLINE=3101687; PubMed=1465456;  RA Screaton G.R., Bell M.V., Jackson D.G., Cornelis F.B., Gerth U.,  RA Bell J.I.;	RESULT 1  CD44 HUMAN  CD44 HUMAN  STANDARD;  PRT;  742 AA.  1D -CD44 HUMAN  STANDARD;  AC P16070; P22511; Q04858; Q13419; Q13957; Q13958; Q13959; Q13960;  AC Q13961; Q13967; Q13988; Q13980; Q15861; Q16064; Q16065; Q16066;  AC Q13961, Q16522; Q06524; Q16064; Q16065; Q16066;  AC Q16208; Q16522; Q06524; Q16064; Q16064; Q16065; Q16066;  AC Q15208; Q16528; Q16528; Q16064; Q16065; Q16066;  AC Q16208; Q16528; Q16528; Q16064; Q16065; Q16066;  AC Q16208; Q16528; Q16528; Q16066; Q16066; Q16066; Q16066; Q16068; Q16066; Q16068; Q16068; Q16068; Q16068; Q16068; Q16068; Q16068; Q16066; Q16068; Q160
RT "Genomic structure of DNA encoding the lymphocyte homing receptor RT CD44 reveals at least 12 alternatively spliced exons."; RL Proc. Natl. Acad. Sci. U.S.A. 89:12160-12164(1992). RN [2] RP SEQUENCE FROM N.A. (ISOFORM EPIDERMAL).	01-NOV-1997 (Rel. 35,

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"Novel variants of CD4
the CD44 alternative s
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SEQUENCE FROM N.A. (ISOFORMS SHORT-TAILED HEMATOPOIBTIC AND C SEQUENCE FROM N.A. (ISOFORMS SHORT-TAILED HEMATOPOIBTIC AND C MEDLINE=89168435; Pubmed=2466576;
MEDLINE=89168435; Pubmed=2466576;
Goldstein L.A., Zhou D.F.H., Picker L.J., Minty C.N., Bargat:
Ding J.F., Butcher E.C.;
"A human lymphocyte homing receptor, the hermes antigen, is to cartilage proteoglycan core and link proteins.";
Cell 56:1063-1072(1989).
                    Hofmann M., Ku
                          TISSUE=Lung;
MEDLINE=92005448; PubMed=1717145;
Hofmann M., Rudy W., Zoeller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stamenkovic I., Amiot M., Pesando J.M., Seed B.;
"A lymphocyte molecule implicated in lymph node homing the cartilage link protein family.";
Cell 56:1057-1062(1989).
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MEDLINE=22388257; PubMed=12477932;
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MEDLINE=89168434;
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hyaluronidase.";
G. 7:212-220(1993).
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                                                                                                                                                                                                                 cartilage;
ens J.W., Buckwalter J.A.,
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A NATIONAL PRODUCTS:

RT J. Biolod group-related polymorphism of CD44 abolishes a hyaluronan-RT binding consensus sequence without preventing hyaluronan binding.";

RI J. Biol. Chem. 271:7147-7153(1996).

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MEDLINE=22038351; PubMed=12032545;

Legg J.W., Lewis C.A., Parsons M., Ng T.,

"A novel PKC-regulated mechanism controls
directional cell motility.";
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MEDLINE=94198700; PubMed=8148709;
Matsumura Y., Hanbury D., Smith J., Tarin
"Non-invasive detection of malignancy by i
CD44 gene activity in exfoliated cancer ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOSYLATION AND PROCESSING. MEDLINE=22766015; PubMed=12883358;
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MEDLINE=98248445; PubMed=9580567;
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MEDLINE=92017823; PubMed=1922057;
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n of CD44 is repressed in neuroblastoma
Biol. 11:5446-5453(1991).
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Best Local Similarity 66.3
----hem 492; Conservative
                                                                                                                            p14745;
p1.4PR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 14, Last sequence update)
17-MAR-2004 (Rel. 14, Last sequence update)
17-MAR-2004 (Rel. 14, Last sequence update)
18-MAR-2004 (Rel. 14, Last sequence update)
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                     Papio hamadryas (Hamadryas baboon).
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Papio.
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Pred. No. 2.5e-146;
1; Mismatches 0;
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                                Vertebrata, Euteleostomi, 
i; Cercopithecidae;
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CONFLICT
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Similarity 68.: 37; Conservative

Score 1698.5; DB 1, Pred. No. 7.7e-99; 7; Mismatches 17;

DB

1;

Indels Length

133;

Gaps

39378 68.2%;

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-> V (IN REF. 1; 578BFCE7C3D52FFF

AA SEQUENCE). CRC64;

25. 57 100 110 120 120 256 67 AA;

25 100 110 120 120 256

SIMILARITY)

N-LINKED (G)

D (GLCNAC . . .)
GLCNAC . . .)

(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)

326

326

PHOSPHORYLATION (PARTIAL)

SIMILARITY)

BY SIMILARITY

BY SIMILARI

PYRROLIDONE CARBOXYLIC ARG/LYS-RICH (BASIC)

ACID

(PROBABLE).

PHOSPHORYLATION (BY PKC) (PARTIAL)

YB)

MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEXNGRYSISRTEAADLCKAFNSTL

PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTYCFN MDKFWWRAAWGLCLVQLSLAQIDLNITCRFEGIYHVEKNGRYSISRTEAADLCKAFNSTL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 66-74.

MEDLINE=89382830; PubMed=2471974;

Idzerda R.L., Carter W.G., Nottenburg C., Wayner E.A.,

Gallatin W.M., St John T.;

Gallatin W.M., St John T.;

"Isolation and DNA sequence of a cDNA clone encoding a
"Isolation and DNA sequence of a cDNA clone encoding a
                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00658; CD44.
PRINTS; PR01265; LINKMODULE.
PRODOm; PD000918; LINK; 1.
SMART; SM00445; LINK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                          Proteoglycan; Signal; Alternative Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                     PROSITE; PS01241; LINK; 1. Cell adhesion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M22452; AAA35385.1; -. HSSP; P98066; 1TSG.
                                                                                                                                                                                                                                                     Pyrrolidone
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001231; CD44 antigen.
InterPro; IPR000538; Link.
                                                                                                                                                                                                                                    HAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lymph node homing.

SUBCELLULAR LOCATION: Type I membrane protein.

PTM: Extensively modified including N- and O-linked glycosylation, addition of the glycosaminoglycan chondroitin sulfate, of sulfate, of phosphate to cytoplasmic domain serine residues.

SIMILARITY: Contains 1 link domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00193; Xlink; 1.
         21
21
270
291
291
225
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                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                          CD44 ANTIGEN.
EXTRACELLULAR
                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                             Glycoprotein;
tive splicing;
                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       Phosphorylation;
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Third Mouse Standard; PRT; 778 AA.

215379, Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408; Q62409; Q64296; Q99114; Q90XX8; Q61409; Q64296; Q99114; Created)

10-OCT-2003 (Rel. 14, Created)

15-MAR-2004 (Rel. 42, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

CD44 antigen precursor (Phagocyttic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte)

(Extracellular matrix receptor) (Hermes antigen) (Hyaluronate receptor)
the primate cDNA.".
Proc. Natl. Acad. 8
[4]
                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 13).

MEDLINE=9003849; PubMed=2681416;
Zhou D.F.H., Ding J.F., Ficker L.J., Bargatze R.F., Butcher E.

Goeddel D.V.;

"Molecular cloning and expression of Pgp-1. The mouse homolog
human H-CAM (Hermes) lymphocyte homing receptor.";

J. Immunol. 143:3390-3395(1989).
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).

STRAIN=DBA/2; TISSUE-Lung;

MEDLINE=93107170; PubMed=1469058;

MEDLINE=93107170; PubMed=1469058;

"He Q., Lesley J., Hyman R., Ishihara K., Kincade P.W.;

"Molecular isoforms of murine CD44 and evidence that the membry proximal domain is not critical for hyaluronate recognition.";

Droximal domain 1s not critical for hyaluronate recognition.";

Cell Biol. 119:1711-1719(1992).
                                                                         MEDLINE=90046829; PubMed=2682651; Nottenburg C., Rees G., St John T. "Isolation of mouse CD44 cDNA: sti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETRNLQNVDMKIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVNSRRRCGQKKKLVINNGNGAVEDRKSSGLNGEASKSQEMVHLVNKESSETPDQFMTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQEMTAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPN
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Rodentia;
                           U.S.A.
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Sciurognathi; Muridae;
                           86:8521-8525(1989)
                                                                            structural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               the membrane
                                                                               distinct
                                                                                                                                                                                                                                                                                                         В.С.,
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                                                                                                                                                                                                                                                                                                 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Sihimi I.M., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Balake J.A., Rapadt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Blake J.A., Rapadt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., RA Gasterland T., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Kanai A., Kwaji H., Kawasawa Y., Kedzierski R.M., King B.L., RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., RA Konagaya A., Waltais L., Marchionni L., McKenzie L., Miki H., RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., RA Petrovsky W., Pillai R., Pontius J.U., Qi D., Ramachandran S., RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Ra Sandelin A., Schneider C., Semple C.A., Sebcu W., Shimada X., Varardo R., Watanabe Y., Wells C., Wang Y., Watanabe Y., Wells C., RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang J., Yang L., Yang L., Yang J., Yang J.
     REPLINE=22388257, PubMed=12477932;

RAMEDLINE=22388257, PubMed=12477932;

RAMEDLINE=2388257, PubMed=1247932;

RAMEDLINE=238825, PubMed=2388257, PubMed=1247932;

RAMEDLINE=238825, PubMed=
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MEDILINE=20318634; PubMed=10859330;

Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guenthert

"Abrogation of experimental colitis correlates with increased
apoptosis in mice deficient for CD44 variant exon 7 (CD44v7).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 13).
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis
J. Exp. Me
                                                                                                                                                   August
                                                                                                                                                        SEQUENCE OF 8-778 FROM N.A. (ISOFORM 13).
MEDLINE=90094420; PubMed=2403559;
WOLIFE B.J., Gause W.C., Pelfrey C.M., Holland
August J.T.;
                                                                         surface antigen
J. Biol. Chem. 2
                                                                            "The cDNA sequence of mouse Pgp-1 and homology to huma surface antigen and proteoglycan core/link proteins."; J. Biol. Chem. 265:341-347(1990).
                                SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exp. Med. 191:2053-2064 (2000)
                                                                                                                                                                                                                                                                                   full-length cDNAs.";
420:563-573(2002).
                                224-637
                                FROM
                                N.A.
                                (ISOFORMS
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а́н., ЧТ.,

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6

to human S.M.,

Steinberg A.D.,

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Name=12; Synonyms=M1;
IsoId=p15379-3; Sequence=VSP_005328;
Name=13; Synonyms=M0;
IsoId=p15379-2; Sequence=VSP_005329;
IsoId=p15379-2; Sequence=VSP_005329;
-i- PTM: N-glycosylated (By similarity).
-i- PTM: O-glycosylated; contains chondroitin sulfate glycans which can be more or less sulfated (By similarity).
-i- PTM: Phosphorylated; activation of PKC results in the dephosphorylation of Ser-742 (constitutive phosphorylation site), and the phosphorylation of Ser-708 (By similarity).
-i- POLYMORPHISM: Two allelic forms of this glycoprotein, PGP-1.1 and PGP-1.2, have been reported. The expressed product is PGP-1.1 (Ly-24.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=93286043; PubMed=8509359;
Screaton G.R., Bell M.V., Bell J.I., Jackson D.G.;
The identification of a new alternative exon with highly restricted
tissue expression in transcripts encoding the mouse Pgp-1 (CD44)
homing receptor. Comparison of all 10 variable exons between mouse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A new alternatively spliced exon between v9 and v10 provides a molecular basis for synthesis of soluble CD44.";
J. Biol. Chem. 271:20603-20607(1996).
-i- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion mucosal high endothelial venule and to types I and VI collagen. Probably involved in matrix adhesion, lymphocyte activation and lymph node homing.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toelg C., Hofmann M., Herrlich P., Ponta "Splicing choice from ten variant exons variability.";
Nucleic Acids Res. 21:1225-1229(1993).
[9]
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93219085; PubMed=8464707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 268:12235-12238(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q., Toole B.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=4; Synonyms=M2;
IsoId=P15379-4; Sequence=VSP_007331;
                                                                                                                        SIMILARITY: Contains 1 link domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ime=7; Synonyms=M4;
IsoId=P15379-6; Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 me=6; Synonyms=M3;
IsoId=P15379-5; Sequence=VSP_005326;
                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P15379-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P15379-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P15379-9; Sequence=VSP_007332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P15379-8; Sequence=VSP_007330;
                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P15379-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P15379-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P15379-14; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence=VSP_005327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence=VSP_007329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence=VSP_007332,
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Best Local S
Matches 370
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EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M30655; AAA39922.1; -..., M27129; AAA37406.1; -..., M27130; AAA37407.1; -..., M27151594; CAB61888.1; -..., AZ2515594; CAB61888.1; -..., AC05676; AAH05676.1; -..., AK045226; BAC32269.1; -..., J05163; AAA39923.1; -..., X69724; CAA49380.1; -..., X69724; CAA49380.1; -..., L13611; AAA37145.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLPTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYIL-TSNTSQYDTY
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VINGGNGTVEDRKPSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSVDMKIGV
                                                                        SDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKL
                                                                                                              HTKESRTFIPVTSAKTGSFGVTAVTVG-DSNSNVNRSLSGDQDTFHPSGGSH--TTHGSE
                                                                                                                                                 POSHSONFSTLHGEPEEDENYPTTSILPSSTKSSAKDARRGGSLPTDTTTSVEGYTFQYP
                                                                                                                                                                           OGSNSOS PSTSHEGLEEDKOHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHYP
                                                                                                                                                                                                   EDVSW-TDFFDPISHPMGQGHQTESKDTDSSHSTTLQPTAAPNTHLVEDLNRTGPLSVTT
                                                                                                                                                                                                                                                     TSTTPNSTAEAAATQQETWFQNGWQGKNPPTPSEDSHVTEGTTASAHNNHPSQRITTQSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHNASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDD
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                     VINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADETRNLQNVDMKIGV
                                                 LAGHSSANQDSGVTTTSGPMRRPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKL
                                                                                                  DIMENGILEPVIPAKTEVFGETEVILAIDSNVNVDGSLPGDRDSSKDSRGSSRIVTHGSE
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CAA46882.1; -.
CAA46881.1; -.
CAA46880.1; -.
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47.4%; Pred. No. 3.6
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                                                                                                                                                                                                                             ----PATNMDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTT
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RESULT 4
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EMBL; U10881; AAA19316:1; -.
HSSP; P98066; 1TSG:
InterPro; IPR001231; CD44 antigen.
InterPro; IPR000538; Link.
Pfam; PF00193; X11nk; 1.
PRINTS; PR00658; CD44.
PRINTS; PR01265; LINKMODULE.
PRODOM; PR01265; LINKMODULE.
PRODOM; PR01265; LINKMODULE.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 35, Last annotation update)
16-MAR-2004 (Rep. 1) (R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
MOD_RES
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SIGNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                    Cell adhesion; Transmembrane; Glycoprotein; Proteoglycan; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Heparan sulfate proteoglycan) (HAM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q60522-2; Sequence=VSP_005322;
PTM: N-glycosylated (By similarity).
PTM: O-glycosylated; contains chondroitin sulfate glycans w
can be more or less sulfated (By similarity).
PTM: Phosphorylated; activation of PKC results in the
dephosphorylation of Ser-395 (constitutive phosphorylation
and the phosphorylation of Ser-361 (By similarity).
SIMILARITY: Contains 1 link domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymph node homing.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
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                                                                       BY SIMILARITY.
CD44 ANTIGEN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
LINK.
                               STEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2)
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Best Local Simi
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Similarity 67.5%;
37; Conservative
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                                                                                                                                                                                                                                                                                                                                            MDKFWHHAAWGLCLLFLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCQAFNS
                                                                                                                                                                                        LAVCIAVNSRRRCGQKKKLVINSGNGAVEDRKÞSGLNGEASKSQEMVHLVNKESSETPDQ
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                                                                                                                                                                                                                                                                                                                       PNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRD
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N-LINKED (GLCNAC. . .) (POTENTIAL).

TRSGGKDGRRGGGLEVENDATISLEGYTHY PETMENGTITPV

TPAKTGVFGETEVTVAEDSNFNVDGSLPG -> R (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
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Pred. No. 1.5e
28; Mismatches
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BY SIMILARITY.
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SIMILARITY).
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CD44 HORSE STANDAKU;

CD44 HORSE STANDAKU;

Q05078;

Q05078;

Q1-FEB-1994 (Rel. 28, Created)

Q1-FEB-1994 (Rel. 28, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

CD44 antigen precursor (Phagocytic Glycoprotein I) (PGP-1) (HUTC (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte (Extracellular matrix receptor) (Hermes antigen) (Hyaluronate receptor)

(PGP-1) (HUTCH-I)

Equus caballus (Horse). Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Perissodactyla; Equidae; Equus. NCBI\_TaxID=9796;

Euteleostomi;

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Query Match
Best Local S
Matches 312
                                                                                                                                                                                                                                                                                                                                               HSSP; P98066; 1TSG.
InterPro; IPR001231; CD44 anti
InterPro; IPR000538; Link.
Pfam; PP00193; Xlink; 1.
PR.NTS; PR01058; CD44.
PR.NTS; PR01265; LINK/ODULE.
PRODOM; PD000918; Link; 1.
SMART; SM00445; LINK; 1.
                                                                         CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                           DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X66862; CAA47331.1; -. PIR; I46245; S24240.
                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                               Cell adhesion;
                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01241; LINK; 1.
                               al Similarity
312; Conserv
MDKFWHHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL
                                 Conservative
                                                                                                                                                                                                                                                                                                           carboxylic acid.
                                                                                                                                                323
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Signal; Alternative
                                                                                                                                                323
                                          59.3%;
                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 antigen.
                                 20;
                                                                        N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
BE20461C587AA34B CRC66
                                          Score 1547; DB Pred. No. 2e-89;
                                                                                                                                                                                                                                                                          BY SIMILARITY.
CD44 ANTIGEN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                        SIMILARITY).
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PHOSPHORYLATION (PARTIAL) (BY
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BY SIMILARITY.
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                                                                                                                                                                      PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                    Glycoprotein; Phosphorylation; Receptor;
tive splicing;
                                Mismatches
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                                 25;
                                                                                                                                                                      (BY PKC) (PARTIAL)
                                                    Length 359;
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01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)	LT 6 CANFA COD44 CANFA STANDARD; PRT; 351 AA.	345 DETRILONVOMKIGV 359	479 DETRNIQNYDMKIGV 493	285 IAVNSRRKCGQKKKLVINNGNGAVDDKKASGLNGEASRSQEMVHLVNKESSETQDQFWTA 344	GNGAVEDRKPSGLNGEAS	232AQTTHGSETSGHSTGSQEGGASTTSGPIRRPQIPEWLIILASLLALALILAVC 284	359 TFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPTRTPQTPEWLIILASLLALALILAVC 418	232 231	299 NHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQD 358	224	239 NTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDP 298	181 GSSSER-STSGGYSIFHTHLPTTRPTQDQSSPWVSDSPEKTPTT 223	181 GSSSERSSTSGGY-IFYT-FSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANP 238	121 ASAPPEEDCTSVIDLPNAFEGPITITIVNRDGTRYTKKGEYRTNPEDINPSTPADDDVSS 180	121 ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 180	61 PTWAQMQKALNIGFETCRIGFIEGHVVIPPIHPNSICAANNTGVYILTSNTSQYDTYCFN 120	61 PTWAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTYCEN 120	1 MDKFWWRAAWGLCLVPLSLAQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCKAFNSTL 60

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SUBCELLULAR LOCATION: Type I membrane protein.

PTM: Extensively modified including N- and O. sulfate, of sulfate, addition of the glycosaminoglycan chondroitin sulfate, of sulfate, of phosphate to cytoplasmic domain serine residues.

SIMILARITY: Contains 1 link domain.

Davis W., Butcher G.W.; "Molecular cloning of equine CD44 cDNA by a COS cell expression

Tavernor A.S., Deverson Davis W., Butcher G.W.,

PubMed=8436424;

E.V.,

Coadwell W.J.,

Lunn

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Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                            CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lym
homing/adhesion receptor) (Hermes antigen) (Hyaluronate
                                                                                              Canis familiaris
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SEQUENCE FROM N.A.

SEQUENCE FROM A.T...

STRAIN=Beagle; TISSUE=Thymus;

MEDLINE=94250687; PubMed=75.14890;

MEDLINE=94250687; PubMed=75.14890;

Milde K.F., Alejandro R., Mintz D.H., Pastori R.L.;

Milde K.F., Alejandro R.L.;

Milde K.F., Alejandro R., Mintz D.H., Pastori R.L.;

Milde K.F., Alejandro R.L.;

Milde K.F., Alejandro

lymph node homing.
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Lymph nodes.
TISSUE SPECIFICITY: Lymph nodes.
PTM: Extensively modified including N- and O-linked glycosylation, addition of the glycosaminoglycan chondroitin sulfate, of sulfate, of phosphate to cytoplasmic domain serine residues (By similarity).
SIMILARITY: Contains 1 link domain.

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PRINTS; PRO1265; LINKWODULE.

PRODOM; PD000918; Link; 1.

PROSITE; PS01241; LINK; 1.

PROSITE; PS01241; LINK; 1.

Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;

Cell adhesion; Signal; Alternative splicing;
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NON TER
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PIR; S45305; S45305.
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InterPro; IPR000538; Link.
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                                                                                                                                                                                                                                          ALSVGFETCRYGFIEGHVVIPRIQPNAICAANHTGYYILISNTSQYDTYCFNASAPPEED
                                                                                                                                                    TSGGYIFYT-FSTVHPIPDEDSFWITDSTDRIPATNMDSSHSTTLQPTANPNTGLVEDLD
                                                                                                                                                                                                   CTSVTDLPNAFDGFITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSS
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                                                                                                  RTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTL
                                                                                                                               SAGYNIFHTHLPTAYPTEDQDSSRVSSNSDHTPIT
                                                                                                                                                                                     CTSVTHLPNAFDGPITITIVNRDGTRYSOKGEYRTNPEDINPSNPTDDDVSSGSSERST
                                             LEGYTSHYPHTKESRTF1PVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTFHPSGGSH
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Pred. No. 1.2e-
21; Mismatches
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR
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GECNAC...
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.2e-84;
es 31; Indels 132;
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InterPro; IPRO01231; CD44_antigen.
InterPro; IPRO01238; Link.
Pfam; PF001293; Xlink; 1.
PRINTS; PR00158; CD44.
PRINTS; PR01265; LINKWODULE.
PRODOm; PD000918; Link; 1.
SMART; SM00445; LINK; 1.
SMART; SM00445; LINK; 1.
PROSTITE; PS01241; LINK; 1.
PROSTITE; PS01241; LINK; 1.
Cell adhesion; Transmembrane; Glycop:
Proteoglycan; Signal; Alternative sp.
Pyrrolidone carboxylic acid.
POTENTI:
SIGNAL 21 366 CD44 ANTICOMETRICAL COMETRICAL COMETRIC
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01-NOV-1997
01-NOV-1997
15-MAR-2004
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CD44
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92017904; PubMed=1922105;
BOSWOTTH B.T., St John T., Gallatin W.M., Harp J.A.;
BOSWOTTH B.T., St John T., Gallatin W.M., Harp J.A.;
"Sequence of the bovine CD44 CDNA: comparison with human
sequences.";
sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD44.
EMBL; X62881; CAA44675.1; -.
EMBL; X62881; AAB20016.1; -.
PIR; A53286; A53286
HSSP; P98066; 1TSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                              SÜBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Mesenteric lymph node and liver, not in heart.
PTM: Extensively modified including N- and O-linked glycosylation,
addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
of phosphate to cytoplasmic domain serine residues (By
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Immunoi. 28:1131-1135(1991).
FUNCTION: Main cell surface receptor for hyaluronate. Adhesion mucosal high endothelial venule and to types I and VI collagen probably involved in matrix adhesion, lymphocyte activation and
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 link domain.
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POTENTIAL. CD44 ANTIGEN

Glycoprotein; ive splicing;

Phosphorylation;

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RESULT 8
CD44 RAT
CD44 RAT
CD46
AC P264
AC 01-N
DT 01-N
DT 15-N
DT 15-N
DE CD44
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Matches 305
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MOD_RES
CD44 RAT STANDARD; PRT; 503 AA.

P26051; Q99021;
01-MAY-1992 (Rel. 22, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDTFWWRAAWGICLVQLSLAQIDLNITCRYAGVFHVEKNGRYSISKTEAADLCKAFNSTL
                                                                                                                                                          QFMTADETRNLQNVDMKIGV
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N-LINKED (GI
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BY SIMILARITY.
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1469.5;
Pred. No. 1.4
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ARG/LYS-RICH (BASIC).

STEM.

PYRROLIDONE CARBOXYLIC ACID
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PHOSPHORYLATION (PARTIAL)
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CYTOPLASMIC
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         HSSP; 598066; 1TSG.
InterPro; IPR001231; CD44 antigen.
InterPro; IPR000538; Link.
InterPro; IPR000538; Link.
Pfam; Pr00193; Xlink; 1.
PRINTS; PR01265; LINKMODULE.
PRINTS; PR01265; LINK; 1.
PRODOM; PD000918; Link; 1.
SMART; SM00445; LINK; 1.
PROSITE; PS01241; LINK; 1.
PROSITE; PS01241; LINK; 1.
Cell adhesion; Transmembrane; Glycop Proteoglycan; Signal; Alternative sp
        DOMAIN
TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
Stevens J.W., Midura R.J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-1. FUNCTION: Main cell surface receptor for hyaluronate.
-1. mucosal high endothelial yenule and to types I and VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91191552; PubMed=1707342;
Guenthert U., Hofmann M., Rudy W., Reber S., Zoeller M.,
Haussmann I., Matzku S., Wenzel A., Ponta H., Herrlich P.;
"A new variant of glycoprotein CD44 confers metastatic potrat carcinoma
                                                                                                                                                                                                                                                      EMBL; M61875; AAA53532.1; -.
EMBL; M61874; AAA53534.1; -.
EMBL; U52179; AAA67915.1; -.
EMBL; U46957; AAA92920.1; -.
PIR; B38745; B38745.
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BDIX; TISSUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazo
Mammalia; Eutheri
NCBI_TaxID=10116;
                                                                                Pyrrol:
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>+</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homing/adhesion receptor) (LY-24).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1; Synonyms-short; Isode-PSP 005330; Isode-P26051-2; Sequence-VSP 005330; PTW: N-glycosylated (By similarity). PTW: N-glycosylated; contains chondroitin sulfate glycans were can be more or less sulfated (By similarity). Phosphorylated; activation of PKC results in the dephosphorylated; activation of FKC results in the dephosphorylation of Ser-467 (constitutive phosphorylation and the phosphorylation of Ser-433 (By similarity). SIMILARITY: Contains 1 link domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probably involved in matrix adhesion, lymphocy lymph node homing.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2; Synonyms=Long, Meta-1; IsoId=P26051-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Metazoa;
Butheria;
                                                                                                        carboxy
         4111
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2384
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Da; Chordata;
la; Rodentia;
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        LINK.
ARG/LYS-RICH
STEM.
                                          CD44 ANTIGEN.
EXTRACELLULAR (POTENTIA
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                    Glycoprotein;
tive splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphocyte
                      (BASIC)
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                                                                       (POTENTIAL)
                                                                                                                                Phosphorylation; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       onate. Adhesion tand VI collagen. sactivation and
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122 100 433

PYRROLIDONE CARBOXYLIC BY SIMILARITY. BY SIMILARITY.

ACID

(PROBABLE).

CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) CD44.

PHOSPHORYLATION (BY PKC) SIMILARITY).

(PARTIAL)

YB)

MOD\_RES

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CRIGR
CD444;
P20444;
01-FEB-1991
01-OCT-1996
15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDKFWWHAAWG-LCLVPLSLA--QIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTLPTMAQMELALRKGPETCRYGFIEGHVVIPRIHPNAICAANNTGVYILLASNTSHYDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STLPTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYI-LTSNTSQYDT
                                                                                                                                                                                               SGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADETRNLQNVDMKIGV
                                                                                                                                                                                                                                       RMT-
                                                                                                                                                                                                                                                                                                                                     SRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTF----HPSGGSHTTHGSESDG
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                                                                                                                                                                                                                                                                                                                                                                                                                         DHPTTSTLTSSNRNDVTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTQWNPIHSNPEVLLQTTTR-----MTDIDRNSTSAHGENWTQEPQPPFNNHEYQDEEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIPATNMDSSHSTTLQPTANPNTGLVEDLDR--TGPLSMTTQQSNSQSFSTSHEGLEEDK 275
                                                                                                                                                                  SGNGTVEDRKPSELNGEASKSQEMVHLVNKEPTETPDQFMTADETRNLQSVDMKIGV
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(Rel. 17, Created)
(Rel. 34, Last seq
(Rel. 43, Last ann
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                                                                          STANDARD;
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55945 MW;
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N-LINKED (GLCNAC. ...) (POTENT
 : sequence up
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/FTId=VSP 005330.
R -> S (IN REF. 2).
FB489D009BD4EE22 CRC64;
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                         PRINTS; PRO0658; CD44.
PRINTS; PRO1265; LINKXODULE.
PRODOM; PD000918; LINK; 1.
SMART; SM00445; LINK; 1.
PROSITE; PS01241; LINK; 1.
Cell adhesion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;

"CD44 is the principal cell surface receptor for hyaluronate.";

Cell 61:1303-1313(1990).

-I- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
mucosal high endothelial venule and to types I and VI collagen.

Probably involved in matrix adhesion, lymphocyte activation and
lymph node homing.
-I- SUBCELIULAR LOCATION: Type I membrane protein.
-I- INDUCTION: By IBV
-I- PTM: Extensively modified including N- and O-linked glycosylation,
addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
of phosphate to cytoplasmic domain serine residues.
-I- SIMILARITY: Contains I link domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cricetulus griseus (
Enikarvota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M33827; AAA36967.1; -. PIR; A35616; A35616. HSSE; P98066; ITSG.
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MEDLINE=90304889;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001231; CD44_antigen.
InterPro; IPR000538; Link.
Pfam; PF00193; Xlink; 1.
                                                                                                                                                                                    MOD_RES
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SIGNAL
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                                                                                                                                                                                                                       MOD_RES
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102
112
112
174
256
39775
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kovic I., Melnick M., Underhill
cipal cell surface receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Chinese hamster).
; Chordata; Craniata; Vertebrata; Euteleostomi;
; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                 362
290
290
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121
160
269
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                               ž
                                       BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PHOSPHORYLATION (PARTIAL) (
SIMILARITY).

PHOSPHORYLATION (PARTIAL) (
SIMILARITY).

N-LINKED (GLCWAC. .) (POT

N-LINKED (GLCWAC. .) (POT
                                                                                                                                                                                                                                                                                                                                                                          CD44 ANTIGEN.
EXTRACELLULAR (POTENTIA
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
tive splicing;
                               E89EB434E9EEC948
                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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177

121 117 망

Query Match Best Local S Matches 315

CONFLICT SEQUENCE

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63 58

RESULT
CD44\_CH
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437 387 377 354 321 295 276 240 218 181

447

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Similarity

Score 1398.5; Pred. No. 3.56

.5e-80

DB 1;

Length

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D. SERI BOWN.

AC p07856;

DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sericin precursor (Silk gum protein).

OS Bombyx mori (Silk moth).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycropoda; Bombycidae; Bombyx.
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Matches 291
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SEQUENCE FROM N.A.
TISSUE-Middle silk gland;
MEDLINE-83082839; PubMed-6294094;
MEDLINE-83082839; PubMed-6294094;
Okamoto H., Ishikawa B., Suzuki Y., "Structural analysis of sericin genes. Homologies in the 5' flanking nucleotide sequences.";
J. Biol. Chem. 257:15192-15199(1982).
                                                            SEQUENCE OF 317-354 FROM N.A.
MEDLINE=87076763; PubMed=3024742;
Michaille J.J., Couble P., Prudhomme
"A single gene produces multiple seri
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ilarity 58.4%;
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sericin mes
                                                              C., Garel A.;
messenger RNAs
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EMBL; J01030; -; NOT ANNOTA

EMBL; J01031; -; NOT ANNOTA

EMBL; J01032; -; NOT ANNOTA

EMBL; J01033; -; NOT ANNOTA

EMBL; J01033; -; NOT ANNOTA

EMBL; J01034; -; NOT ANNOTA

EMBL; M26101; AAA27843.1; -

EMBL; M26102; AAA27844.1; -

S11k; Signal.
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Pred. No. 0.00036;
55; Mismatches 131;
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SERICIN.
; BA605BC0305EAF19
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Oryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Craniata; Ve Mammalia; Eutheria; Lagomorpha; Leporidae;

Vertebrata;

Euteleostomi;

Oryctolagus

P98065;

P98065;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Tumor necrosis factor-inducible protein TSG-6 precursor stimulated gene 6 protein) (Hyaluronate-binding protein TNFAIP6 OR TSG6 OR PS4

RABIT

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InterPro; IPRO00538; Link.
Pfam; PF00431; CUB; 1.
Pfam; PF00193; Xlink; 1.
PFAM; PF00193; Xlink; 1.
PFAM; PF00195; Link; 1.
SMART; SM00041; CUB; 1.
SMART; SM00044; LINK; 1.
SMART; SM00045; LINK; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01181; LINK; 1.
PROSITE; PS01241; LINK; 1.
PROSITE; PS01241; LINK; 1.
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J. Biol. |
[2]
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J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feng P., Liau G.;
"Identification of a novel serum and
"ascular smooth muscle cells.";
vascular smooth c68:9387-9392(1993).
J. Biol. Chem. 268:9387-9392(1993).
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STRAIN=New Zealand white;
MEDLINE=93252803; PubMed=
Feng P., Liau G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M86381; AAA03342.1; -. PIR; A48055; A47290. HSSP; P98066; 1TSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94012707; PubMed=8407990;
Feng P., Liau G.;
J. Biol. Chem. 268:21453-21453(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Possibly involved in cell-cell and cell-matrix interactions during inflammation and tumorgenesis. TISSUE SPECIFICITY: Vascular smooth muscle cells. DEVELOPMENTAL STAGE: Fetal.
INDUCTION: By serum and growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 1 link domain. SIMILARITY: Contains 1 CUB domain.
                        136
 152
                                                 95
                                                                          89
                                                                                                                           3
                                                                                                                                                                Similarity
                                                                                                                         AGVFHVE-KNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFETCRYGFI-EGHVVI
PNEYDDNQICYWHIRLKYGQRIHLSFLNFDLEYDPGCLADYVEIYDSYDDVHGFVGRYCG
                                                 PRIHPUSICAANNIGVY---ILISNISOYDTYCFNASAPPEEDCISV
                                                                                                   AGVYHREARSGKYKLTYABAKAVCEFEGGRLATYKQLEAARKIGFHVCAAGWMAKGRVGY
                                                                                                                                                                                                      53
135
58
82
135
188
118
258
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                                                                                                                                                                                                                                                                                                                                                Signal; Glycoprotein.
1 19 POTENTIAL
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LINK.
CUB.
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BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC...
N-LINKED (GLCNAC....
N-LINKED (GLCNAC....
                                                                                                                                                   Score 171; DB 1;
Pred. No. 0.00055;
4; Mismatches 64
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                          -GTRYVQ------KGEYRT
                                                                                                                                                                             Length 276;
                                                                                                                                                                                                          CRC64;
                                                                                                                                                       Indels
                                                                                                                                                                                                                     (POTENTIAL)
                                                                              68;
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15-MAR-2004 (Rel. 43, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific protein) (CSPCP).
AGGI OD AGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=88087070; PubMed=3693370;
Doege K., Sasaki M., Horigan E., Hass
"Complete primary structure of the ra
protein deduced from cDNA clones.";
J. Biol. Chem. 262:17757-17767(1987).
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1856-2124 FROM N.A. MEDLINE=86250698; PubMed=2424893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: Two globular domains, G1 and G2, comprise the amino terminus of the proteoglycan, while another globular region, (makes up the COOH terminus. G1 contains link domains and thus consists of three disulfide-bonded loop structures designated the A, B, B' motifs. G2 is similar to G1. The keratan sulfate and the chondroitin sulfate (CS) attachment domains lie between pym; Contains mostly chandrain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 N--PEDIYPSNPTDDDVSSGS-----SSERSSTSGGYIFYTFSTYHP
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, Sasaki M., Horigan E., Hassell
Chem. 263:10040-10040(1988).
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                   SEO
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ne rat cartilage proteoglycan
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MBL outstation -
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                                                              Query Match
Best Local S
Matches 99
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PROSITE; PS00615; C_TYPE_LECTIN_1

PROSITE; PS50041; C_TYPE_LECTIN_2

PROSITE; PS50835; IG_LIKE; 1.

PROSITE; PS00290; IG_MIC; 1.

PROSITE; PS00290; IG_MIC; 1.

PROSITE; PS01241; LINK; 4.

Glycoprotein; Proteoglycan; Lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR01265; LINKWODULE.
PRODOM; PD000918; Link; 4.
SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003324; s
InterPro; IPR003436;
                                                                                                                                          CARBOHYD
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InterPro;
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PF00059; lectin_c; 1.
PF02339; SGXXSG; 55.
                       48
                                                                , 66
                                                                                    Similarity
EAADLCKAFNSTLPTMAQMEKALSIGFETCRYGFI-EGHVVIPRIHPNSICAANNTG---
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268
504
602
1910
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ilarity 20.0%;
Conservative 5
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                                                                                                                                              AA;
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3480
3480
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6554
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Ig_W.
Ig_v.
Lectin_C.
Link.
SGXXSG.
Sushi_SCR_CCP.
                                                                                                                                        IG-LIKE V-TYPE.
LINK 1.
LINK 2.
LINK 3.
LINK 4.
C-TYPE LECTIN.
SUSHI.
G1-B.
G1-B.
G2-B.
G2-B.
G2-B.
G2-B.
G2-B.
G2-B.
G2-B.
G2-B.
CS-1.
CS-2.
BY SIMILARITY.
                                                              55
;
                                                            Score 168; DB 1; I
Pred. No. 0.012;
5; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
AGGRECAN CORE PROTEIN.
                                                                                                 Length 2124;
                                                              Indels
                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                              168;
                                                              Gaps
                         103
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RESULT
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                 "Coding sequence, exon-intron structure and chromosoma of murine TNF-stimulated gene 6 that is specifically e expanding cumulus cell-occyte complexes."; Gene 202:95-102(1997).

-I- FUNCTION: Possibly involved in cell-cell and cell-interactions during inflammation and tumorgenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O08859;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor-inducible protein TSG-6
                                                                                                                                                                                                                                                                                STRAIN=CD-1; TISSUE=Cumulus cell, Embryo, MEDLINE=99087423; PubMed=9427551; Fueloep C., Kamath R.V., Li Y., Otto J.M., Glant T.T., Hascall V.C.;
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Stimulated gene 6 protein).
TNFAIP6 OR TNFIP6 OR TSG6.
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE
                                                                                                       similarity).

DEVELOPMENTAL STAGE: Expressed in currence expansion in vivo.

SIMILARITY: Contains 1 link domain.

SIMILARITY: Contains 1 CUB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIPV--TSAKTGSFGVTAVT-VGDSNSNVNRSLSGDQD-TFHPSGGSH---TTHGSESDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGESLEGSASASGTGDLSGLPSGGEITETSASGTEEISGLPSGGDDLETSTSGIDGASVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNMDSSHSTTLOPTAN----PNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLPSGDLDSSGLGPTVSSGLPVESGSASG------DGEIPWSSTPTVDRLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETTEVPYFTTEPEKQTEWEPAYTPVGTSPLPGIPPTWLPTVPAAEEHTESPSASQEPSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYLYPNQTGLPDPLSKHHAFCFRGVSVVPSPGGTPTSPSDIEDWIVTRVEPGVDAVPLEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391
                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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moved. Usage by and for commercial (See http://www.isb-sib.ch/announce)

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Best Local S
Matches 63
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Pfam; PF00193; X11nK;
PFARINTS; PR01265; LINKWODULE.
ProDom; PD000918; Link; 1.
SWART; SM00445; LINK; 1.
SWART; SM00445; LINK; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01241; LINK; 1.
                                                                                                                                                             TLT 14

TIGG HUMAN STANDARD; PRT; 277 AA.

TSG6 CONTROL OF TRES 196 (Rel. 33, Created)

O1-FEB-1996 (Rel. 33, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Tumor necrosis factor-inducible protein TSG-6 precursor stimulated gene 6 protein) (Hyaluronate-binding protein)

TNFAIP6 OR TSG6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
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CARBOHYD
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PIR; JC6506; JC6506.
HSSP; P98066; ITSG.
SEQUENCE FROM N.A.
TISSUE=Fibroblast;
MEDLINE=92112993; PubMed=1730767;
                                                                                                 Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1195266; Tnfaip6.
InterPro; IPR000859; CUB.
InterPro; IPR000538; Link.
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Metazoa; Chordata; C
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Pred. No. 0.0017;
4; Mismatches 70
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REMBL; M31165; AAB00792.1; -.

REMBL; AJ421518; CAD13434.1; -.

REMBL; BC030205; CAD12353.1; -.

REMBL; BC030205; AAH330205.1; -.

REMBL; BC030205; AAH330205.1; -.

REMBL; BC030205; AAH330205.1; -.

REMBL; BC030205; AAH30205.1; -.

REMBL; BC030205; AAH30205.1; -.

REMBL; BC030205; AAH30205.1; -.

REMBL; BC030205; Ficell adhesion receptor activity; TAS

REMIN; BC03005540; Fivell acid binding; TAS.

REMIN; BC030005540; Fivell acid binding; TAS.

REMO; GC300005540; Firell adhesion receptor activity; TAS

REMIN; BC030005540; Firell adhesion receptor activity; TAS

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REQUENCE FROM N.A.

REDINE=22388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Balkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S., Krywinski M.I., Skalska U., Smailu
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MEDLINE=21975206; PubMed=11854277;
Nentwich H.A., Mustafa Z., Rugg M.S., Mahoney D.J., Jenkins S.C., Dowling B.,
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J. Cell Biol. 116:545-557(1992).
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MEDLINE=96390850; PubMed=8797823;

Kohda D., Morton C.J., Parkar A.A., Hatanak

Kohda D., Morton C.J., Parkar M.A., Hatanak

Campbell I.D., Day A.J.;

"Solution structure of the link module: a h

involved in extracellular matrix stability
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Loughlin J., Day A.J.;
"A movel allelic variant of the human TSG-6 gene acid difference in the CUB module. Chromosomal lc frequency analysis, modeling, and expression.";
J. Biol. Chem. 277:15354-15362(2002).
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FUNCTION: Possibly involved in ce interactions during inflammation interactions during inflammation INDUCTION: By TNF.
SIMILARITY: Contains 1 link domaint in the containt of the containt in the containt
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SMART; SM00445; LINK; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS011241; LINK; 1.

Cell adhesion; Signal; Glycoprotein; Pc
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mucin 1 precursor (Polymorphic epithelial mucin)
MUC1 OR MUC-1.
SEQUENCE FROM N.A.

MEDILINE=91330029; PubMed=1714452;

Spicer A.P., Parry G., Patton S., Gendler S.J.;

Spicer A.P., Parry G., Patton S., Gendler S.J.;

"Molecular cloning and analysis of the mouse homologue of the tumor-
associated mucin, MUC1, reveals conservation of potential O-
glycosylation sites transmembrane, and cytoplasmic domains and a
loss of minisatellite-like polymorphism.";

J. Biol. Chem. 266:15099-15109(1991).
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CARBOHYD
VARIANT
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                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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ProDom; PD000918; Link; 1.
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Pfam; PF00193; Xlink; 1.
                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                             MOUSE
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InterPro; IPR000859;
InterPro; IPR000538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 6.2%;
Similarity 33.3%;
40; Conservative ;
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N-LINKED (GLCNAC.
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R-> Q.
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Pred. No. 0.0019;
1; Mismatches 50;
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LINK.
CUB.
                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                            PRT;
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    EMBL; M84683; AAA39756.1; EMBL; U16175; AAA98538.1; -
EMBL; M65132; AAA39755.1; -
EMBL; M64928; AAA39755.1; -J
EMBL; M77226; AAA39754.1; -
FMRL; A93344; A33944
PIR; A39344; A39344
PIR; I52257; I52257.
MGD; MGI:97231; MGCI.
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SIGNAL
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SEQUENCE FROM N.A.
MEDLINE=92068178; P.
Vos H.L., Devries Y.
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vos H.L., Devries Y., Hilkens J.;
Vos H.L., Devries Y., Hilkens J.;
"The mouse episialin (Mucl) gene and its promoter:
the repetitive domain in the protein.";
Biochem. Biophys. Res. Commun. 181:121-130(1991).
                                                                                                                                                                        REPEAT
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Pfam; PF01390; SEA; 1.
SMART; SM00200; SEA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: DIRECT OR INDIRECT INTERACTION WITH ACTIN
CYTOSKELETON.
SUBCELILLAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCLUSIVELY L
IN THE APICAL DOMAIN OF THE PLASMA MEMBRANE OF HIGHLY
POLARIZED EPITHELIAL CELLS.
TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF EPITHELIAL
TISSUE SPECIFICITY: EXPRESSED IN EPITHELIAL CARCINOWAS.
TISSUES, ABERRANTLY EXPRESSED IN EPITHELIAL CARCINOWAS.
PYM: HIGHLY O-GLYCOSYLATED AND PROBABLY ALSO N-GLYCOSYLATED.
SIMILARITY: CONTAINS 1 SEA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50024;
 PubMed=1958179;
 SEA_domain.
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 SEA.

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16.
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CYTOPLASMIC (POTENTIAL).

16 X 20 AA TANDEM APPROXIMATE REPEATS
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EXTRACELLULAR (POTENTIAL).
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(APPROXIMATE)
                                                                                                                                                                                                                                                             (APPROXIMATE).
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                           promoter:
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               (POTENTIAL)
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Search completed: March 8, 2004, 06:08:51
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                    126 SSPVVHSGTSSA-----ATTAPVDSTSSPVVHGGTSS-PATSPPGDSTSSPDHSSTSSP 178
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                                                                                                                                                                  239 SP----ATSPLRDSTSSPVHSSASIQNIKTTSDLASTPDHNGTSVTT--TSSALGSATS 291
                                                                                                                                                                                                                                                                                       239 NTGLVEDLDRTGPLSMTTQQSNSQSF-STSHEGLEEDKDHPTTSTLTSSNRNDVT-GGRR 296
                                                                                 292
                                                                                                                     355 GDQDTFHPSGGSHTTHGSES 374
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                                                                                                                                                                                                        297 DPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTS--AKTGSFGVTAVTVGDSNSNVNRSLS 354
                                                                                                                                                                                                                                                                                                                                                                                                                     77 TRAPEDSTS-TAVLSGTSSPATTAPVN-SASSPVAHGD-----TSSPATSPLKDSN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 IEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTYCFNASAPP--------
                                                                            PDH-----SGTSTTTNSSES 306
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138 139 AT -> PA (IN REF. 2).
140 140 T -> TT (IN REF. 2).
423 423 F -> S (IN REF. 2).
506 506 S -> D (IN REF. 2).
630 AA; 64622 MW; FF57C1B31137CB3B CRC64;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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# ALIGNMENTS

OS Homo sapiens (Human).  OC Homo sapiens (Eutheria; Pr  OC Mammalia; Eutheria; Pr  OC NCBI_TAXID=9606;  [1]  RN FI TISSUE=COlon adenocarc  RA Wiebe G.J., Freund D.,  RI "Sequence analysis of  RI "Sequence analysis of  RI Submitted (Apr-2002) t  EMBL; AY101192; AAM500  DR GO; GO:0016020; C:memb  GO; GO:0016020; C:memb  GO; GO:0007155; P:cell  DR GO; GO:0007155; P:cell  DR InterPro; IPR001231; C  DR InterPro; IPR001231; C  DR InterPro; IPR001231; C  RI Ffam; PF00193; Xlink;  PRINTS; PR01265; LINK;  PROSSITE; PS01241; LINK;  RR PROSSITE; PS01241; LINK;  RR PROSSITE; PS01241; LINK;  RR SEQUENCE 493 AA; 53	PESOLITION OF THE PESOLITION O	186Z27 E 86Z27; 1-JUN-2003 ( 1-JUN-2003 ( 1-JUN-2003 ( 1-OCT-2003 (
ia; Metazoa; Chordata; Craniata; ia; Hetazoa; Chordata; Catarrhini ia; Eutheria; Primates; Catarrhini iz; Colon adenocarcinoma; i=Colon adenocarcinoma; G.J., Freund D., Corbeil D.; nce analysis of the human CD44 ant ted (APR-2002) to the EMBL/GenBank AY10119; AAM50040.1; 10016020; C:membrane; IEA. 10016020; C:membrane; IEA. 1000540; F:cell adhesion receptor 10005540; F:cell adhesion; IEA. 10007155; F:cell adhesion; IEA. 1007155; F:cell adhesion; IEA. 1007157; F:cell adhesion; IEA. 1007157	01-JUN 01-JUN 01-OCI CD44 a CD44.	n 🛱 n
NCBI TAXID=9606; [1] SEQUENCE FROM N.A. SIGUENCE FROM N.A. TISSUB-colon adenocarcinoma; TISSUB-colon adenocarcinoma; TISSUB-colon adenocarcinoma; TISSUB-colon adenocarcinoma; TISSUB-colon adenocarcinoma; TISSUB-colon adenocarcinoma; TS-colon CD44 antigen." Sequence analysis of the human CD44 antigen." Sequence analysis of the human CD44 antigen." GO; GO:0016020; C:membrane; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:00015540; F:cell adhesion receptor activ GO; GO:000540; F:hyaluronic acid binding; IEA. GO; GO:000155; F:cell adhesion; IEA. InterPro; IFR00123; CD44_antigen. InterPro; IFR00123; CD44_antigen. InterPro; IFR00123; Kink; 1. PRINTS; PR01265; LINK; 1. PRINTS; PR01265; LINK; 1. SMART; SM00445; LINK; 1. PROSITE; PS01241; LINK; 1.		sapiens (Human). ryota; Metazoa; Chordata; alia; Eutheria; Primates;
TISSUE-COION ademocarcinoma; Wiebe G.J., Freund D., Corbeil D.; Wiebe G.J., Freund D., Corbeil D.; "Sequence analysis of the human CD44 ant Submitted (Apr-2002) to the EMBL/GenBank EMBL, AY101192; AAM50040.1; GO; GO:0016020; C:membrane; IEA. GO; GO:0004895; F:cell adhesion receptor GO; GO:0005540; F:hyaluronic acid bindin GO; GO:0007155; P:cell adhesion; IEA. InterPro; IPR001231; CD44 antigen. InterPro; IPR000538; Link. PRINTS; PR00658; CD44. PRINTS; PR00658; CD44. PRINTS; PR00658; LINK, 1. PROSITE; PR00658; LINK; 1. SMART; SM00445; LINK; 1. PROSITE; PS01241; LINK; 1. PROSITE; PS01241; LINK; 1. PROSITE; PS01241; LINK; 1.		
	יינו	TISSUE=Colon adenocarcinoma;
	¥ 5	Wiebe G.J., Freund D., Corbeil D.;
	22	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
GO; GO:0004895; GO; GO:000540; GO; GO:0007155; InterPro; IPR001 InterPro; IPR001 Pfam; PR00193; PRINTS; PR00658; PRINTS; PR01265; PRODOM; PD010918 SMART; SM00445; PROSITE; PS01241 SEQUENCE 493 A	DR DR	AAM50040.1; C:membrane;
GO; GO:0005540; GO; GO:0007155; InterPro; IPR001 InterPro; IPR000 Pfam; PR00193; X PRINTS; PR00658; PRINTS; PR01265; PRODOM; PD010918 SMART; SM00445; PROSITE; PS01141 SEQUENCE 493 A	DR	GO:0004895;
InterPro; IPR001231; CD44_antig InterPro; IPR00558; Link. Pfam; PF00193; Xlink; 1. PRINTS; PR0058; CD44 PRINTS; PR01265; LINKMODULE. PRODOm; PD000918; Link; 1. SMART; SM00445; LINK; 1. PROSITE; PS01241; LINK; 1. PROSITE; PS01241; LINK; 1. SEQUENCE 493 AA; 53398 MW;	ᅜ	GO:0005540;
InterPro; IPR000538; Link. Pfam; PF00193; X1ink; 1. PRINTS; PR00658; CD44. PRINTS; PR01265; LINKMODULE. PRODom; PD000918; Link; 1. SMART; SM00445; LINK; 1. PROSITE; PS01241; LINK; 1. SEQUENCE 493 AA; 53398 MW;	뮸	erPro;
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PRINTS; PRO1265; LINKWODULE. PRODOM; PD000918; Link; 1. SMART; SM00445; LINK; 1. PROSITE; PS01241; LINK; 1. SEQUENCE 493 AA; 53398 MW;	뮸	PR00658;
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Matches 492; Conserv
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GO; GO:0016020; C:nembrane; IEA.

GO; GO:0004895; F:cell adhesion receptor ac

GO; GO:0005540; F:hyaluronic acid binding;

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IPR000131; CD04 antigen.

InterPro; IPR000538; Link.

Pfam; PF00139; Xlink; 1.
                                                                                                              PRINTS; PRO0658; CD44.
PRINTS; PRO1865; LINKMODULE.
PRODOM; PD000918; LINK; 1.
SMART; SM00445; LINK; 1.
PROSITE; PS01241; LINK; 1.
SEQUENCE 699 AA; 76628 MW;
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Q96J24;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
Similar to CD44 antigen (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; BC004372; AAH04372.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Pancreas;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Primates;
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                         95.5%;
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19, Last sequence update)
25, Last annotation update)
(Homing function and indian
Score 2490; DB 4;
Pred. No. 1.5e-168;
1; Mismatches 0;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ68Dl8.2.5 (CD44 antigen (Homing function and indian system)) (Fragment).
   Cobley V.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ datab EMBL, AL13330; CAC10346.1; -.
HSSP, P98066; 1TSG.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004895; F:cell adhesion receptor activity;
GO; GO:0005540; F:hyaluronic acid binding; IEA.
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local S
Matches 469
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InterPro; IPR001238; Link.
Pfam; PF00123; Xlink; 1.
PRINTS; PR001265; CD44.
PRINTS; PR01265; LINKWODULE.
PRODOM; PD000918; LINK; 1.
SMART; SM00445; LINK; 1.
PROSITE; PS01241; LINK; 1.
NON TER
SEQUENCE 470 AA; 50727 MW; E4B47
                                                                                                                                                                                                                                                                                                               Q9UJ36 PRELIMINARY; PRT; 742 AA.
Q9UJ36;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transmembrane glycoprotein precursor.
SEQUENCE FROM N.A.

MEDLINE=94147793; PubMed=7508842;

Gunthert U.;

"CD44: a multitude of isoforms with diverse functions.";

Curr. Top. Microbiol. Immunol. 184:47-63(1993).

EMBL; AJ251595; CAB61878.1; -.
                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                Submitted
                                                                                                                                                                     SEQUENCE FROM N.A. Gunthert U.;
                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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Pred. No. 4.5e-167;
O; Mismatches 1;
                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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GG; GG:0016020; C:membrane; IEA.

GG; GG:0004895; F:cell adhesion receptor activity; IE;

GG; GG:0004895; F:cell adhesion; IEA.

GG; GG:0005540; F:hyaluronic acid binding; IEA.

GG; GG:0007155; P:cell adhesion; IEA.

InterPro; IFR00123; CD44 antigen.

InterPro; IFR000538; Link.

InterPro; IFR000538; Link.

PRINTS; PR0058; CD44

PRINTS; PR0058; CD44

PRINTS; PR01265; LINKWODULE.

PRODC; SM00445; LINK; 1.

SMART; SM00445; LINK; 1.

PROSITE; PS01241; LINK; 1.
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPAT-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTYCFN
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                                                                    ALILAVCIAVNSRRRCGOKKKL
                                                                                                         ALILAVCIAVNSRRRCGOKKKLVINSGNGAVEDRKPSGLNGEASKSOEMVHLVNKESSET
                                                                                                                                                  SLSGDOTTHPSGGSHTTHGSESDGHSHGSQEGGANTTSGFIRTPQIPEWLIILASLLAL
                                                                                                                                                                       SLSGDQDTFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLAL
                                                                                                                                                                                                                                                         TGGRRDPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNR
                                                                                                                                                                                                                                                                                                          LQPTANPNTGLVENLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKOHPTTSTLTSSNRNDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDFISSTISTTPRAFDHTKQNQDWTQWNPSHSNPEVLLQTTTRMTDVDRNGTTAYEGNWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AWDWFSWLFLPSESKNHLHTTTQMAGTSSNTISAGWEPNEENEDERDRHLSFSGSGIDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTYNTSQYDTYCFN
                                                                                                                                                                                                                               TGGRRDPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNR
                                                                                                                                                                                                                                                                                                                                                                                                                                     -------NMDSSHSTT
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742 AA;
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742 1
81598 MW;
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Pred. No. 3.2e-166;
2; Mismatches 1;
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TRANSMEMBRANE GLYCOPROTEIN.
; C319E5CE5C0B51D3 CRC64;
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Best Local S
Matches 468
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P CODIES V.;

CODIES V.;

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AL13330; CAC10345.1; -.

R HSSP; P98066; ITSG.

R GG; GG:0016020; C:membrane; IEA.

R GG; GG:0004895; F:cell adhesion receptor activity; IEA.

R GG; GG:0007155; P:cell adhesion; IEA.

R GG; GG:0007155; P:cell adhesion; IEA.

R InterPro; IPR001231; CD44_antigen.

R InterPro; IPR001231; CD44_antigen.

R InterPro; IPR001231; CD44_antigen.

R PRINTS; PR01658; CD64.

R PRINTS; PR01658; CD64.

R PRINTS; PR01659; CD64.

R PRINTS; PR01659; LINKWODULE.

R PRODOM; DR000445; LINK; 1.

R PRODOM; DR000445; LINK; 1.
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Q9H5A7,
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ68D18.2.4 (CD44 antigen (Homing function and indian blood group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   system)) (Fragment). CD44.
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                                                                                                                                                                                                                                                                                                                                          TISTTPRAFDHTKQNQDWTQWNPSHSNPEVLLQTTTRMTDVDRNGTTAYEGNWNPEAHPP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYIFYTFSTVHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFETCRYGFIE
   PNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRD
                                    PNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRD
                                                                                                                 AAASAHTSHPMQGRTTPSPEDSSWTDFFNPISHPMGRGHQAGRRMDMDSSHSITLQPTAN
                                                                                                                                                                                                                            LIHHEHHEEEETPHSTSTIQATPSSTTEETATQKEQWFGNRWHEGYRQTPKEDSHSTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPDEDSPWITDSTDRIPATSTSSNTISAGWEPNEENEDERDRHLSFSGSGIDDDEDFISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676 AA; 73929 MW; 122C7250B7DA0F47 CRC64;
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                                                                                                                                                                     -----NMDSSHSTTLQPTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 2348; DB 4; Length 676; 69.2%; Pred. No. 1.7e-158; tive 1; Mismatches 1; Indels 206;
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                                             297
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204 IPDEDSPWITDSTDRIPAT 222	84 GHVVIPRHENSICAANTGVYILTSNTSQYDTYGNASAPPEBDCTSVTDLPNAFDGFI 143	ry Match 89.2%; Score 2326.5; DB 4; Length 719; t Local Similarity 65.1%; Pred. No. 6.3e-157; t Local Similarity 65.1%; Pred. No. 6.3e-157; the A6B; Conservative 1; Mismatches 1; Indels 249; Gaps ches 46B; Conservative 1; Mismatches 1; Indels 249; Gaps 24 LNITCREAGVEHVEKNGRYSISRTBAADLCKAFNSTLPTMAQMEKALSIGESTCRYGFIE 83	I.P.A. sion receptor activity; IEA. c acid binding; IEA. sion; IEA. ntigen. ntigen.	CD44.  thomo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  MAGNI TAXID=9806;  [1]  SEQUENCE FROM N.A.  Cobley V.;  Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.  EMBL; AL133330; CAC10347.1;  HSSP; P98066; 1TSG.	A5 A5 Q9H5A5 Q9H5A5 PRELIMINARY; PRT; 719 AA. Q9H5A5, Q1-MAR-2001 (TrEMBLrel. 16, Created) Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update) Q1-MAR-2003 (TrEMBLrel. 25, Last annotation update) D1-0CT-2003 (TrEMBLE) D16BD18-2.3 (CD44 antigen (Homing function and indian blood group system)) (Fragment).	478 ADETRNIQNYDMKIGV 493                 661 ADETRNIQNYDMKIGV 676	298 PNHSEGSTILLEGYTSHYPHTKESRTFIPVTSAKTGSPGVTAVTVGDGNISNYNRSLISGDQ 357  481 PNHSEGSTILLEGYTSHYPHTKESRTFIPVTSAKTGSPGVTAVTVGDGNISNYNRSLISGDQ 540  358 DTFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAV 417

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                                                                                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0004895; F:cell adhesion receptor activity; IEA.
GO; GO:000546; F:hyaluronic acid binding; IEA.
GO; GO:0005155; P:cell adhesion; IEA.
InterPro; IPR001231; CD44 antigen.
InterPro; IPR001231; CD44 antigen.
InterPro; IPR000538; Link;
InterPro; IPR000538; Link;
InterPro; IPR00193; Xlink; 1.
PRINTS; PR00195; CD44.
PRINTS; PR01255; LINKNODULE.
PRODOm; PD000918; Link; 1.
SMART; SM00445; LINK; 1.
INCOMPANY INCO
                                                                                                                             Query Match
Best Local Similarity
Matches 426; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Chondrosarcoma;
Stevens J.W., Midura R.J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ
EMBL; U46959; AAA92921.1.;
EMBL; U46959; AAA92921.1.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q62913 PRELIMINARY; PRT; 514 AA. Q62913; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) CD44i (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                                                                                                                                                                                                                             514 AA; 55647 MW;
                                                                                                                        84.0%;
illarity 82.9%;
Conservative ?
                                                                                                                        Score 2189.5; DB 11
Pred. No. 2.2e-147;
1; Mismatches 0;
                                                                                                                                                                                                                                37A4984F0E3DDA92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- NMDSSHSTTLOPTANPNTGLVEDLDRTGPLSM
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                                                                       Query Match
Best Local S
Matches 359
                                                                                                                                                                    Ansorge W., Krieger S., Newes H.W., Wei.
Osanger A., Wiemann S.;
Submitted (Apr-2003) to the EMEL/GenBanl
EMBL; Al832642; CAD89965.1; -.
GO; GO:0016920; C:membrane; IEA.
GO; GO:0005840; F:Cell adhesion receptor
GO; GO:0005540; F:Myalluronic acid bindir
GO; GO:0007155; P:Cell adhesion; IEA.
InterPro; IPR000531; CD44 antigen.
InterPro; IPR000538; Link.
PFINTS; PR01265; LINK, 1.
PRINTS; PR01265; LINKNODULE.
PTODOM; PD000918; Link; 1.
SMART; SM00445; LINK; 1.
SMART; SM00445; LINK; 1.
PROSITE; PS01241; LINK; 1.
PROSITE; PS01241; LINK; 1.
PROSITE; PS01241; LINK; 1.
SMART; SM00445; LINK; 1.
SMART; SM0045; LINK; 1.
SMART; SM0145; LINK; 1.
SMART; SM0145; LINK; 1.
SMART; SM0145; LINK; 1.
SMART; SM0145; LINK; 1.
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01-JUN-2003 (TrEMBLrel. 25, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Hypothetical protein DKFZp451K1918.
DKFZP451K1918
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Q86T72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                     Similarity
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                                                                            Conservative
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                                                                                               70.4%;
72.8%;
                                                                       Score 1837; DB 4;
Pred. No. 1.6e-122;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                               F51A746B44387C54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor activity;
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240 279 180

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300 223 180

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180

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RESULT
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                        Query Match
Best Local Sim
Matches 359;
                                                                                                      TISSUE-Normal pigmented retinal epithelium;
Wiebbe G.J., Freund D., Corbeil D.;
Wiebbe G.J., Freund D., Corbeil D.;

"Sequence analysis of the human CD44 antigen.";

Submitted (Apr.2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY101193; AAM50041.1; -.

R GO; GO:00016020; C:membrane; IEA.

R GO; GO:0004895; F:cell adhesion receptor activity; IEA.

R GO; GO:0007155; P:cell adhesion; IEA.

R GO; GO:0007155; P:cell adhesion; IEA.

R GO; GO:0007155; P:cell adhesion; IEA.

R InterPro; IPR001231; CD44 antigen.

R InterPro; IPR001231; CD44 antigen.

R Ffam; PR00193; X1ink; 1.

R PFAINTS; PR00165; LINK; 1.

R PFAINTS; PR01265; LINK; 1.

R PFODOm; PD000918; Link; 1.

R PROSITE; PS01241; LINK; 1.

R PROSITE; PS01241; LINK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pu
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8N694;
01-OCT-2002
01-OCT-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD44 antigen. CD44.
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2 (TrEMBLrel.
3 (TrEMBLrel.
                             Conservative
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Primates;
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Last sequence update)
Last annotation update)
                          0
                        Score 1835; DB 4; Length 361; Pred. No. 2.2e-122; O; Mismatches 2; Indels 13
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Q80X37;
01-JUN-2003
01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q80X37
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Sciurognathi; Muridae; Murinae; Mus
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Best Local S
Matches 368
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EMBL; BC051388; AAH51388.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004895; F:cell adhesion receptor activity;
GO; GO:0005540; F:hyaluronic acid binding; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR001231; CD44 antigen.
InterPro; IPR001231; Link.
Pfam; PF00193; Xlink; 1.
PRINTS; PR00658; CD44.
PRINTS; PR00658; CD44.
PRINTS; PR00658; LINKNODULE.
ProDom; PD000918; LINK; 1.
PROSITE; PS01265; LINK; 1.
PROSITE; PS01241; LINK; 1.
 Q9H5A4;
Q9H5A4;
01-MAR-2001
01-MAR-2001
01-OCT-2003
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Salivary gland;
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Similarity 63.2%;
68; Conservative 36
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                                                                                                                                                                    GEASKSQEMVHLVNKESSETPDQFMTADETRNLQNVDMKIGV
                                                                                                                                                                                                            FGVTAVTVG-DSNSNVNRSLSGDQDTFHPSGGSH--TTHGSESDGHSHGSQEGGANTTSG
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                                                                                                                                                                                                                                                                                                                                                                                                          QGHQTESKDTDSSHSTTLQFTAAPNTHLVEDLNKTGPLSVTTPQSHSQNFSTLHGEPEED
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                                                                                                                                                GEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSVDMKIGV
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                                                                  PRELIMINARY;
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25,
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Created)
Last sequence update)
Last annotation update)
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es 85; Indels
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CD44.
   008779;
008779;
01-JUL-1997 (
01-JUL-1997 (
01-OCT-2003 (
CD44 protein.
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Cobley V.
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Query Match
Best Local S
Matches 337
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GO; GO:0004895; F:cell adhesion receptor activity; IE

GO; GO:0005480; F:hyaluronic acid binding; IEA.

GO; GO:0005540; F:hyaluronic acid binding; IEA.

InterPro; IPRO01231; CD44_antigen.

InterPro; IPRO01231; CD44_antigen.

PRINTS; PRO01231; Xink; 1.

PRINTS; PRO1058; CD44.

PRINTS; PRO1058; LINKMODULE.

PRODOM; PRO1058; LINK; 1.

ROSITE; PSO1141; LINK; 1.

PROSITE; PSO1441; LINK; 1.

PROSITE; PSO1441; LINK; 1.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2000) to the EMBL; AL133330, CAC10348.1; HSSP; P98066; ITSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.4%;
al Similarity · 71.7%;
337; Conservation
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FIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTFHPSGGSHTTHGSESDGHSHGSQE
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338 AA; 36732 MW;
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Primates;
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Pred. No. 3.5e-113;
0; Mismatches 1;
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Catarrhini; Hominidae;
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25, 25,

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Best Local S
Matches 370
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PRINTS; PRO1265; LINKWODULE.

PRODOM; PD000918; Link; 1.

SMART; SM00445; LINK; 1.

PROSITE; PS01241; LINK; 1.

SEQUENCE 780 AA; 85917 MW;
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HSSP; P98066; I
GO; GO:0016020;
GO; GO:0004895;
GO; GO:0005540;
GO; GO:0007155
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CCD44.

CCD44.

CLATIC NOTVEGICUS (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat

MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BDX; TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Rattus norvegicus CD44 protein sequence.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001231; CD44
InterPro; IPR000538; Link.
Piam; PF00193; Xlink; 1.
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GO:0004895; F:cell adhesion receptor activity;
GO:0005540; F:hyeluronic acid binding; IEA.
GO:0007155; P:cell adhesion; IEA.
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70; Conservative
SHYPHTKESRTFIPVTSAKTGSFGVTAVTVG-DSNSNVNRSLSGDQD-TFHPSGGSHT-T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STLPTMAQMEKALSIGFETCRYGFIEGHVVIFRIHPNSICAANNTGVYI-LTSNTSQYDT
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                                                                                                                                                                                                                                                                             HATSTTWADPNSTTEEAATQKEKWFENEWQGKNPPTPSEDSHVTEGTTASAHNNHPSQRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTKMPGTESNTNPTGWKPNEENEDETDKYPNPSGSGIDDDEDFISSTIATTPWVSAHTK 359
                                                                        SVTTPQSHSQNFSTLPGELEEGEDHPTTSVLPSSTK---SGRRRGGSLPRDTTTSLEGYT
                                                                                                      SMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEGYT
                                                                                                                                                                         TTQSQEDVSWTDFFDPISHPMGQGHQTESKDTGSSHSTTLQPTAAPNTHLVEDLNRTGPL
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47.2%; Pro
ative 35;
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SOURCE STREET TO SOURCE
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097569;
01-MAY-1999 (TREMBLEEL, 1
01-MAY-1999 (TREMBLEEL, 1
01-CCT-2003 (TREMBLEEL, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

WORTLEY M.B.;

White rhinoceros CD44.";

White rhinoceros CD44.";

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases

EMBL; AF045939; AAD02418.1; -.

HSSP; P98066; ITSG.
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GO; GO:0004895; F:cell adhesion receptor ac
GO; GO:0005540; F:chyalluronic acid binding;
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR001231; CD44 antigen.
InterPro; IPR000538; Link.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000918; Link; 1.
SMART; SM00445; LINK; 1.
PROSITE; PS01241; LINK; 1.
NON_TER 364 364
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PRINTS; PR01265; LINKMODULE
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Similarity 64.1%;
18; Conservative 1
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                                                                                                                                                                                                                          ASAPP-EEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEVRTNPEDIYPSNPTDDDVS
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                                                                                                                    SGSSSERSSTSGGY-IFYT-FSTVHPIFDEDSPWITDSTDRIPATNMDSSHSTTLQPTAN
                                                                                                                                                                                     ASAPPGEEDCSSVIDLPNAFEGPITITIVNRDGTRYSKKGEVRTNPEDINPSTQADEDVS
                                            PNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRD
                                                                                           SGSSSER-STSGGYSIFHTHLPTTRPTQDQGSPWVSD-
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Chordata; Craniata; Vertebrata;
Perissodactyla; Rhinocerotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39670 MW;
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10,
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1536.5; DB 6; Length Pred. No. 3.6e-101; 7; Mismatches 26; Indels
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Ceratotherium
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                                    GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005895; F:cell adhesion receptor activity; IE;

GO; GO:0005540; F:byaluronic acid binding; IEA.

InterPro; IPR001231; CD44 antigen.

InterPro; IPR001231; CD44 antigen.

Pfam; PF00193; Xlink; 1.

PFANTS; PR01065; CD44.

R PRINTS; PR01065; LINK*, 1.

R PRODOM; PD000918; Link; 1.

R PRODOM; PD000918; Link; 1.

R PROSITE; PS01141; LINK; 1.

R PROSITE; PS01241; LINK; 1.

R PROSITE; PS01241; LINK; 1.
                                                                                                                                                                                                                                                       "Genomic structure of DNA encoding the lymphocyte homi reveals at least 12 alternatively spliced exons."; Proc. Natl. Acad. Sci. U.S.A. 89:12160-12164(1992). EMBL; IO5423; AABL3622.1; -... EMBL; H05407; AABL3622.1; JOINED. EMBL; L05407; AABL3622.1; JOINED. EMBL; L05407; AABL3622.1; JOINED. EMBL; L05408; AABL3622.1; JOINED. EMBL; L05409; AABL3622.1; JOINED. EMBL; L05420; AABL3622.1; JOINED. EMBL; L05420; AABL3622.1; JOINED. EMBL; L05420; AABL3622.1; JOINED. EMBL; L05420; AABL3622.1; JOINED. EMBL; L05421; AABL3622.1; JOINED. EMBL; L05421; AABL3622.1; JOINED. EMBL; L05421; AABL3622.1; JOINED. EMBL; L05421; AABL3622.1; JOINED.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Lymphoblast;

MEDLINE=92017823; PubMed=1922057;

Shtivelman E., Bishop J.M.;

"Expression of CD44 is repressed in neuroblastoma Mol. Cell. Biol. 11:5446-5453(1991).
                                                                                                                                                                                                                                   EMBL; 105422; AAD....
PIR; JH0417; JH0417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, Cres
01-FEB-1997 (TrEMBLrel. 02, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Cell surface glycoprotein CD44.
                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lymphoblast;
MEDLINE=93101687; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                £98066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                93101687; PubMed=1465456;
G.R., Bell M.V., Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAV 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIAVNSRERCGOKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDOFMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
 57.3%;
68.7%;
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Last annotation update)
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 Score
Pred.
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 No. 2.
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med exons.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cornelia
   DB 4;
.8e-98;
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                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                F.B.,
            Length
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                      Query Match
Best Local
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                                                                                       PRINTS; PR00658; CD44.
PRINTS; PR01265; LINKWODULE.
PRODOM; PD000918; Link; 1.
SWART; SW00445; LINK; 1.
PROSITE; PS01241; LINK; 1.
SEQUENCE 364 AA; 39725 MW;
                                                                                                                                                                                                                               GO; GO:0005540; F:hyeluronic acid bin
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR001231; CD44_antigen.
InterPro; IPR000538; Link.
Pfam; PF00193; Xlink; 1.
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01-AUG-1998 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                     EMBL; AF065147; AAC17117.1; -. HSSP; P98066; ITSG: GO:0016020; C:membrane; IEA. GO; GO:0004895; F:cell adhesion receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein CD44s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    070509
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1998) to the EMBL; AF065147; AAC17117.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stevens J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS
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                      59.2%;
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25,
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Score 1367.5;
Pred. No. 3.6e.
20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                               BA249776C4419AA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
annotation update)
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                         .6e-89;
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                                             DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
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S

MDKFWWHAAWG-LCLVPLSLA--QIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFN

Matches

295;

Conservative

20;

44;

Indels 139;

Gaps

10;

MDKVWWHTAWGLLCLLQLSLAQOQIDLNITCRYAGVEHVEKNGRYSISRTEAADLCEAFN 60   MDKVWWHTAWGLLCLLQLSLAQOQIDLNITCRYAGVEHVEKNGRYSISRTEAADLCEAFN 60   MDKVWWHTAWGLLCLLQLSLAQOQIDLNITCRYAGVEHVEKNGRYSISRTEAADLCEAFN 60   MDKVWWHTAWGLLCLLGCETCRYGFIEGHVVIERIHPNSICAANNTGVYI-LTSNTSQYDT 116   MINIMAL	נ	Qy 4.	Db 28	Qy 4:	Db 2:	Ογ 3:	Db 2:	Qy 2!	Db 20	Qy 2:	Db 16	0γ 1:	Db 12	Ογ 11	Dp e	<b>Q</b> у 5	dd
		476 MTADETRNIQNYDMKIGV 493	VINSGNGTVEDRKPSELNGEASKSQEMVHLVNKEPTETPDQF	-	PRGGFDTVTHGSELAGHSSGNQDSGVTTTSGPARRPQIPEWLIILASLLALALIL	-	LATSDGDSSMD				DLPTSQPT-					8 STLPTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYI-LTSNTSQYDT	

n completed: March 8, 2004, 06:11:38 tme : 50 secs

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Result
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                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                              Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
:
                                                                                                                          Pred. No.

    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

                                                                                                                                                         A_Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
Query
Match
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## ALIGNMENTS

AAU99123 standard; protein; 493 A

AAU99123;

24-SEP-2002 (first entry)

Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.

haematopoietic progenitor cell; stem cell isolation; engraftment; human haematopoietic disorder; leukaemia; inflammatory disorder; stroke; myocardial infarction; Parkinsor; disease; diabetes; muscle dystrophy; liver disorder; rheumatoid arthritis; inflammatory bowel disease. HCELL; haematopoietic cell E-selectin/L-selectin ligand; cancer; asthma human;

Homo sapiens.

WO200244342-A2

06-JUN-2002.

Score

Length

BB

Description Aau99123 Abu04623

Haematopo

100.0

2590 2590 2590 2590

AAW80454 AAW89151 AAY96140

Aaw80454 Aaw89151 Aay96140

ABU04623 ABU04612 AAU99123 Ħ

18-OCT-2001; 2001WO-US051014.

18-OCT-2000; 11-JUN-2001; 2000US-0240987P. 2001US-0297474P.

(BGHM ) BRIGHAM & WOMENS HOSPITAL

Sackstein

WPI; 2002-527707/56.

cancer. New purified hematopoietic cell E-selectin/L-selectin ligand polypeptide useful for treating hematopoietic disorders, inflammatory conditions and

Claim 7; Page 10; 94pp; English.

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AC AC This invention relates to a purified glycosylated polypeptide expressed on normal human haematopoietic progenitor cells and on leukaemic blasts, termed haematopoietic cell E-selectin/L-selectin ligand (HCELL). The HCELL protein of the invention is useful for identifying a stem cell, fo isolating a stem cell from a population of cells or for increasing the engraftment potential of a cell population. The protein is useful for treating a haematopoietic disorder such as leukaemia, or inflammatory disorder in a subject. Methods of the invention are useful for treating haematopoietic disorder in a subject or mammal, and treating cancer or a for

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ABU04613 AAR91445 ABU04631 ABU04621 ABU56470 ABU04647 ABU04614 ABU04614

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ABU04639 ABU04633 ABU04635 ABU04637 ABU04627

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Matches 493;
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                                      Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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The invention describes a purified polypeptide, which comprises a confragment of a kinase, phosphatase, protease, protease inhibitor. The transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a companial an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also composition for class I mfc-binding polypeptide. The polypeptide is also class I or class II mfc-binding polypeptide. The polypeptide and color cancer are particularly useful for treating or preventing class. In mfc-binding polypeptide. The polypeptides and color cancer, gastric cancer, adenocarcinoma, sercoma, melanoma, color cancer, gastric cancer, adenocarcinoma, sercoma, melanoma, color cancer, gastric cancer, adenocarcinoma, sercening agents for treating the above mentioned diseases. This sequence represents an competent protein tag (EPT) isolated from human tissue for translational compositions. Note: This sequence does not appear in the printed composition of the protein content of the polypeptide content and content a

Sequence 493 AA;

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Query Match
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28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
01-OCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358985P.
The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The solveptide is also useful for identifying compounds that binds to a naturally processed class I or class I MHC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MMC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
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Query Match
Best Local S
Matches 493
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                                                                                                                                                                                                                     SEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTF
                                                                                                                                                                                                                                                                                     GLVEDLDRIGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNH
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                                                                                    VNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE
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AAR20817 standard; protein; 493 B

AAR20817;

25-MAR-2003 21-MAY-1992 entry)

Rapid immunoselection cloning technique; cell surface epithelium; tumour invasiveness; carcinoma. Epithelial CD44 Antigen.

Homo sapiens

Modified-site Modified-Domain Peptide -gite 97. .99 /label= N-linked\_glycosylation /label= extracellular 65. .67 Location/Qualifiers /label= N-linked\_glycosylation /note= "putative" /label= signal

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                                                                                           Matches 490;
                                                                                                     Query Match
Best Local :
                                                                                                                                                                     The cDNA encoding epithelial CD44 is quite similar to haematopoietic CD44.5 cDNA (see AAQ21185), but encodes an additional extracellular domain of 165 mino acids, inserted about 140 residues upstream of the transmembrane section shared by both clones. The ability to interfere with binding of epithelial CD44 to extracellular matrices can be useful in diagnostics and therapy, e.g. to diminish the likelihood of metastatic in cancer patients. Soluble forms of CD44 can act to prevent metastatic cells from "homing" to lymph nodes. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                                      CD53 cell surface antigen and DNA encoding it - diagnosis of haematopoietic neoplasms, etc.
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                                                                                                     Similarity
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                                                          MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL
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PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTYNTSQYDTYCFN
                  PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHENSICAANNTGVYILTSNTSQYDTYCFN
                                                                                           Conservative
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/note= "potential site
chondroitin sulphate"
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chondroitin sulphate"
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/label= N-linked_glycosylation
/note= "putative"
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140. .142
/label= N-linked glycosylation
/note= "putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chondroitin sulphate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= N-linked_glycosylation
/note= "putative"
390. .391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= cytoplasmic
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label= glycosylation
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'note= "putative"
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13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
01-DEC-1992;
                                                                                                                                                                               Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CD44 antigen (epithelial form).
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07-JUN-1999
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                                                                                                        WPI; 1998-609251/51.
N-PSDB; AAV63462.
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90US-00553759.
92US-00983647.
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89US-00379076.
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New cloning vector and poly:linker efficient cloning and expression of i
lymphocyte antigenic sequences.

mammalian cDNA(s), especially

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RESULT 6
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ID AAW8
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AC AAW8
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DT 10-M
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Best Local S
Matches 490
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                                                                            standard;
                                                                                                                                                                                                                                                 VNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE
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Pred. No. 2.9e-190;
0; Mismatches 3;
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25-FEB-1988;
13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
01-DEC-1992;
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Amiot M,
                                                                                                                                                                                                                                                            Key
Domain
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                                                                                                                                                                                                                                            US5849898-A
                                                                                                                                                                                                                                                                                      metastasis; therapy.
                                                                                                                                                                                                                                                                                           CD44; cell surface antigen; human; cDNA library; T lymphocyte
                                                                                                                                                                                                                                                                                                      Human CD44 antigen (epithelial form)
                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                   15-DEC-1998
                                                                                                                                                                              (GEHO)
                                                                                                                                                                              GEN HOSPITAL CORP.
                                                                                                                                                               Oquendo C,
Lauffer L,
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90US-00498809.
90US-00553759.
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                                                                                                                                                                                                                                                       /note= "transmembrane
                                                                                                                                                               Camerini
Allen J,
                                                                                                                                                           I D, Summons
                                                                                                                                                                    Stamenkovic I,
                                                                                                                                                               Ö
                                                                                                                                                                Aruffo
                                                                                                                                                                    Stengelin
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cDNA encoding human CD40 antigen - useful for cloning cDNA encoding of surface antigens, constructing cDNA libraries, expressing vectors for expression in eukaryotic cells or their fragments.

1999-069813/06. DB; AAV81219.

Example 15; Col 79-82; 79pp; English.

This polypeptide comprises human CD44 antigen. Its amino acid sequence CC was deduced from the nucleotide sequence (see AAV81219) of a cDNA clone CC isolated from a colon carcinoma HT29 cell library using a novel method CC for cloning cDNAs from mammalian expression libraries. The method is Dased on translent expression of an antigen in eukaryctic cells and copysical selection of cells expressing the antigen by adhesion to an ICC antibody-coated substrate. It is useful for the isolation and cloning of any protein which can be expressed and transported to the cell surface CC membrane of a eukaryctic cell, and was used to clone genes (see AAV81199-CC CD7, CD13, CD14, CD16, CD19, CD20, CD27, CD28, CD31, CD34, CD37, CD37, CD38, CD37, CD38, CD37, CD37, CD38, CD37, CD37, CD37, CD38, CD37, CD37

Sequence 493

AA;

Ş 용 S Matches Query Match Best Local Similarity 490; 13 \_ PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTYCFN MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL Conservative 99.3%; 0 Score Mismatches 2590; DB 2; No. 2.9e-190; Length 493; Indels 0; Gaps 120 60 0

10-MAY-1999

(first

entry)

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121

ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS PTWAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTYNTSQYDTYCFN

180

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RESULT 7
AAY961A9
ID AAY97
AAY961A9
AAY961A9
AC AAY9
AC AAY9
AC AAY9
AC CD44
KW immu
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13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
01-DEC-1992;
                                                 WPI; 2000-586382/55.
N-PSDB; AAA50598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD44.5; cell surface antigen; human; immunoselection; panning; immunodiagnosis; diagnosis; immunotherapy; gene therapy; immune infection; asthma; immune-complax disease; amyloidosis; multiple sclerosis; parasitic disease; epithelial; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human epithelial CD44.
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Isolated nucleic acid molecule encoding
                                                                                                                        Stamenkovic I,
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89US-00379076.
90US-00498809.
90US-00553759.
92US-00983647.
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     the
     CD19
  cell surface antigen,
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useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, particular infections or disorders, e.g. asthma, immune-complex disease, particular infections or disorders, e.g. asthma, immune-complex disease, particular immune-comple parasitic

Example 15; Col 75-78; 75pp; English

The present sequence is that of human epithelial CD44, a glycosylated CC membrane protein that may promote tumor invasiveness. The sequence was CC predicted from a cDNA clone (see AAA50598) isolated by screening a cDNA clone (see AAA50598) isolated by screening a cDNA CD ilbrary prepared from the the colon carcinoma line HT29 using the method CC if the invention. The method, designed to isolate cell surface antigen CC (cSA) nucleic acids, is based upon transient expression of a CSA in CC (cSA) protected cells and physical selection of cells expressing the antigen CC through the color of cells expressing the antigen CC cells and the proteins they encode, are useful for immunodiagnostic and cc culture dish. CSA nucleic acids isolated by the method of the invention, CC and the proteins they encode, are useful for immunodiagnostic and cc immunotherapeutic applications, diseases, and disorders in animals, including the manner. These disorders include asthma, immune-complex disease, amyloidosis, parasitic diseases or multiple sclerosis. The ability to interfere with the binding of epithelial CD44 with extracellular matrices can be useful in diagnostics and therapy. Interference of the binding can diminish the likelihood of metastasis in cancer patients. Soluble forms of CD44 can act to prevent metastatic cells from homing to lymph nodes

Sequence 493 AA;

S 밁 δ 밁 S 문 S 밁 5 뮍 δ 吊 8 밁 Ś 묽 Ś Query Match Best Local & Matches 481 421 361 361 301 301 241 241 181 181 121 121 481 421 6 61 490; ш щ Similarity 99.4 90; Conservative MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL GLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNH PTMAQMEKALSIGFETCRYGFIEGHVVIFRIHFNSICAANNTGVYILISNTSQYDTYCFN VNSRRRCGQKKKLVINSGNGAVEDRKÞSGLNGEASKSQEMVHLVNKESSETÞDQFMTADE HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLILASLLALALILAVCIA HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALIILAVCIA SEGSTHLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTF SEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTF GLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNH GSSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPRTNMDSSHSTTLQPTANPNT GSSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPATIMDSSHSTTLQPTANPNT ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTYNTSQYDTYCFN MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL TRNLONVOMKIGV TRULQUVDMKIGV 493 VNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHL ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 99.3%; Score 2590; DB 3; 99.4%; Pred. No. 2.9e-190; rative 0; Mismatches 3; Length 493; Indels 0, Gaps 300 180 120 120 480 420 420 360 360 300 240 240 180 60 60 480 0

RESULT 8
AAU02449
ID AAU0
XX
AC AAU0

AAU02449 standard; protein;

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AAU02449

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25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
The present sequence encoding for human epithelial antigen CD44 is 1 of various human lymphocyte cell surface antigen polypeptide sequences (AAU02435-AAU02452) described in the present invention. The invention relates to a novel method of cloning cDNA encoding cell surface antigens and efficient construction of cDNA libraries. Also described are 2 expression vectors (AAS03171, AAS03174) which provide high level expression in eukaryotic host cells. A genetically engineered cDNA sequence encoding the CD28 amino acid extracellular domain sequence
                                                                                                                                                                                                                               Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                       New recombinant DNA encoding CD28 useful for diagnosing immune-mediated diseases, infections or disorders, e.g. erythematosus, asthma, transplant rejection, rheumatoid
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                                                                                                                Example 15;
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DB; AAS03192.
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89US-00379076.
90US-00553759.
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390. .391
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/note= "SG dipeptide that site of serine-linked chorn
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site of serine-linked chondroitin sulphate :
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                                                                                                               72pp; English.
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Best Local S
Matches 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
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                                                                             VNSRRRCGQXKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQEMTADE
                                                                                                                     HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIA
                                                                                                                                                 HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIA
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                              TRNLQNVDMKIGV
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ABU04637 standard; protein; 493 ጅ

ABU04637

29-JAN-2003 (first entry)

Human expressed protein tag (EPT) #1303.

RESULT 9
ABU04637
ID ABU0
XX ABU0
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XX Tenma
XX Tran
XX Tran
XX Prott
XW rece
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XX Adem
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

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Matches 490
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                                                                          GLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNH
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; 2001US-0292544P.
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; 2001US-0336370P.
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Pred. No. 2.9e-190;
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21-MAY-2001; 2001US-0292544P.
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01-OCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0326370P.
20-FEB-2002; 2002US-0358985P.
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MG-binding polypeptide. The polypeptides and polymuclectides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational

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  28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
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Query Match

Length 493;

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The invention describes a purified polypeptide, which comprises a configuration of a kinase, phosphatase, protease, protease inhibitor. The cytoskeletal protein, receptor or transcription factor. The colypeptide is useful as an immunogenic composition for eliciting in a manmal an immunogenic response directed against any of the purified polypeptide. The purified protypeptide, or the antibody that binds to this colypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed colypeptide is also useful for identifying compounds that binds to a naturally processed color class II MRC-binding polypeptide. The polypeptide and color cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, colon cancer, gastric cancer, adenocarcinoma for compact for cancer and colon cancer, gastric cancer, adenocarcinoma for compact for cancer, gastric cancer, adenocarcinoma for compact for cancer, gastric cancer, adenocarcinoma for compact for cancer, gastric cancer, adenocarcinoma for cancer, gastric cancer, adenocarcinoma for cancer, gastric cancer, adenocarcinoma, melanoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, colon cancer, gastric cancer, adenocarcinoma for cancer, g
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04-DEC-2001; 2001US-0336780P-
20-FEB-2002; 2002US-0358985P
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멅 8 음 성 밁 Ś 밁 ্ধ 밁 Ś 밁 ঠ 뮍 ঠ 뭐 ঠ Matches 490; Best Local 421 361 361 301 301 241 241 181 181 121 421 121 61 13 **|--3** Similarity MDKFWWHAAWGLCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIA SEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTF GLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNH GLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNH GSSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNT ASAPPEEDCTSVTDLENAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYESNPTDDDVSS PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTYNTSQYDTYCFN PTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTYCFN MDKFWWHAAWGLCLVPLSLAQIDLNITCRPAGVFHVEKNGRYSISRTEAADLCKAFNSTL VNSRRRCGOKKKLVINSGNGAVEDRKFSGLNGEASKSQEMVHLVNKESSETFDQFMTADE HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIA SEGSTHLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTF GSSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPRTNMDSSHSTTLQPTANPNT ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS VNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE Conservative 99.3%; Score 2590; D Pred. No. 2.9e 0; Mismatches 0; DB 6; ?.9e-190; <u>.</u>. Gaps 360 .180 480 480 420 420 240 240 180 120 60 360 300 300 0

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Query Match 99.:
Best Local Similarity 99.4
Matches 490; Conservative
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21-MAY-2001; 2001US-029544P.
08-AUG-2001; 2001US-0310801P.
01-OCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0336780P.
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20-FEB-2002;
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Pred. No. 2.9e-190;
0; Mismatches 3;
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28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
01-OCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358985P.
                                                                                                                                                                                                                                                                                                                                                   Translational profiling; expressed protein tag; EPT; kinase; phosprotease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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New polypeptides (e.g. kinases, phosphatases, proteases, trancytoskeletal proteins, receptors or transcription factors), treating cancer, e.g. colon cancer, gastric cancer, sarcoma, , transporters, rs), useful for coma, lymphoma o ő

Example 2; SEQ ID NO 1279; 134pp; English

The invention describes a purified polypeptide, which comprises a cc fragment of a kinase, photsphatase, protease, protease inhibitor. Cc transporter, cytoskeletal protein, receptor or transcription factor. The cultivaries is useful as an immunogenic composition for eliciting in a cc mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this colypeptide is useful for treating cancer. The polypeptide is also cuseful for identifying compounds that binds to a naturally processed colypeptide or class I MHC-binding polypeptide. The polypeptides and cc class I or class I MHC-binding polypeptide. The polypeptides and cc class I or class I mHC-binding polypeptide. The polypeptides and cc polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for c treating the above mentioned diseases. This sequence represents an completion but was obtained in electronic format directly from WIPO at the proposition but was obtained in electronic format directly from WIPO at fragments or natural characters. ftp.wipo.int/pub/published\_pct\_sequences binds to this

Sequence 493 8

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           PTMAQMEXALSIGFETCRYGFIEGHVVIPRIHÞNSICAANNTGVYILTSNTSQYDTYCFN
                                  MDKTWWHAAWGICLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTL
                                                                         Conservative
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ABU04613

standard;

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                                                                                                                                                                                                                                                                                                                                                                        Cell surface antigen; cloning; immunoselection; immunotherapy; therapy; diagnosis; vector; epithelial CD44 antigen; carcinoma; cancer;
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31-OCT-1996
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/label= Glycosylation_site
97. .99
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Best Local :
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13-JUL-1989;
13-JUL-1990;
01-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The epithelial form of human CD44 antigen (AAR91445) is weakly expressed by normal epithelium but highly expressed by carcinomas. Its amino acid sequence was deduced from a cDNA clone (AAR14725) isolated from colon carcinoma HT29 cells using a novel immunoselection cloning technique. CD44 was produced in transfected COS cells. A haematopoistic form (AAR91444) of CD44 was also identified. The ability to interfere with the binding of epithelial CD44 with extracellular matrices can be useful in diagnostics and therapy; interference of such binding can diminish the likelihood of metastasis in cancer patients. Soluble forms of CD44 can act to prevent metastatic cells from 'homing' to lymph nodes. (Updated or 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seed
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                                                              HPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIA
                                                                                                           SEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSPGVTAVTVGDSNSNVNRSLSGDQDTF
                                                                                                                                                            GLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNH
                                                                                                                                                                                                                GSSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTANPNT
                                                                                                                                                                                                                                                     ASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS-
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                VNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE
                                                 HPSGGSHTTRGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIA
                                                                                             SEGSTHLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDTF
                                                                                                                                           GLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNH
                                                                                                                                                                                           GSSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPRTNMDSSHSTTLQPTANPNT
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  VNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE
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90US-00553759.
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Pred. No. 1.2e-189
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sequence:
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                                                                                                                           2489.5
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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262.213 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd
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10 US-09-927-463-8

14 US-10-156-932-14

14 US-10-052-641-2

9 US-09-909-320-201
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US-10-983-000A-16

15 US-10-116-275-206

16 US-09-870-759-73

10 US-09-871-708A-73

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Sequence 2, Appli
Sequence 16, Appl
Sequence 73, Appl
Sequence 73, Appli
Sequence 73, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 22, Appli
Sequence 27, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 14, Appli
Sequence 2, Appli
Sequence 201, Appli
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## ALIGNMENTS

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Sequence 2, Application US/10012969C
Publication No. US20030108984A1
GENERAL INFORMATION: US2003108984A1
GENERAL INFORMATION: US200310898C
TITLE OF INVENTION: CD44 SPILCE VARIANT ASSOCIATED WITH RHEUMATOID ARTHRITIS
TITLE REFERENCE: COUL21-2
CURRENT FILING DATE: 2002-09-25
CURRENT FILING DATE: 2002-09-25
CURRENT FILING DATE: 2002-09-25
FRIOR FILING DATE: 2002-09-25
FRIOR FILING DATE: 2000-06-07
NUMBER: PATENTION NUMBER: PCT/IL00/00326
FRIOR FILING DATE: 2000-06-07
NUMBER: PATENTION NUMBER: US/10/00326
FRIOR FILING DATE: 2002-09-25
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TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALI:
TITLE OF INVENTION: OF BRAIN TUMORS
FILE REPERBYCE: 263/180 - PEAGLEMAN -- AGY
CURRENT APPLICATION NUMBER: US/09/983,000A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 16
LENGTH: 742
TYPE: PRT
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Publication No. US20030118585A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: AGY Therapeutics
APPLICANT: Melcher, Thorsten
APPLICANT: Mueller, Sabine
APPLICANT: Chin, Daniel
                                                                                                                                                                                                                                                                         NAME/KEY: SIGNAL
LOCATION: (1)..(20)
OTHER INFORMATION: BY SIMILARITY
                                                                                                                              NAME/KEY: CHAIN
LOCATION: (21)..(742)
OTHER INFORMATION: CD44 ANTIGEN
                                                                                                                                                                                                     NAME/KEY: Gene
LOCATION: (1). (742)
OTHER INFORMATION: CD-44 Antigen
                                                               NAME/KEY: DOMAIN
LOCATION: (21)..(649)
OTHER INFORMATION: EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
FEATURE:
                                                KEY: TRANSMEM
ION: (650)..(670)
INFORMATION: POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEE 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CARBOHYD
LOCATION: (548)..(548)
OTHER INFORMATION: N-LINKED (VAME/KEY: CARBOHYD
LOCATION: (599)..(599)
OTHER INFORMATION: N-LINKED (VAME/CONTROL (1999)...(599)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CARBOHYD
LOCATION: (100)...(100)
OTHER INFORMATION: N-LINKED ((
NAME/KEY: CARBOHYD
LOCATION: (110)...(110)
OTHER INFORMATION: N-LINKED ((
NAME/KEY: CARBOHYD
LOCATION: (120)...(120)
COTHER INFORMATION: N-LINKED ((
NAME/KEY: CARBOHYD
                                             NAMB/KEY: VARSPLIC
LOCATION: (224)...(472)
OTHER INFORMATION: MISSING (
NAME/KEY: VARSPLIC
LOCATION: (223)...(223)
OTHER INFORMATION: T -> R (I
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LOCATION: (48)..(119)
OTHER INFORMATION: LINK
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LOCATION: (25)...(25)
OTHER INFORMATION: N-LINKED (GLCNAC
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LOCATION: (671)..(742)
OTHER INFORMATION: CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                     NAME/KEY: VARSPLIC

NAME/KEY: VARSPLIC

OTHER INFORMATION: MISSING (IN ISOFORM WITH ALTERNATIVE SPLICE DONOR/ACCEPTOR
OTHER INFORMATION: MISSING
OTHER INFORMATION: MISSING
OTHER INFORMATION: T -> S (IN ISOFORM WITHOUT EXON 6)

NAME/KEY: VARSPLIC
LOCATION: (223). (266)

OTHER INFORMATION: MISSING (IN ISOFORM WITHOUT EXON 6)

NAME/KEY: VARSPLIC
LOCATION: (224)...(223)
OTHER INFORMATION: T -> N (IN ISOFORMS WITHOUT EXONS 6 TO 11)

OTHER INFORMATION: T -> N (IN ISOFORMS WITHOUT EXONS 6 TO 11)
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LOCATION: (30)...(742)
LOCATION: (30)...(742)
OTHER INFORMATION: MISSING (IN ISOFORM CD448F)
NAME/KEY: VARSPLIC
LOCATION: (192)...(192)
OTHER INFORMATION: G -> A (IN ISOFORM WITH ALT
OTHER INFORMATION: 5)
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OTHER INFORMATION: N-LINKED (GLCNAC ...) (POTENTIAL)
NAME/KEY: VARSPLIC
LOCATION: (23)..(29)
OTHER INFORMATION: DLNITCR -> GVGRRKS (IN ISOFORM CD44SP)
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LOCATION: (350)...(350)
OTHER INFORMATION: N-LINKED (GLCNAC
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LOCATION: (57)...(57)
OTHER INFORMATION: N-LINKED (GLCNAC
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LOCATION: (77)...(97)
OTHER INFORMATION: BY SIMILARITY
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DTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID (PROBABLE)
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OTHER INFORMATION: BY SIMILARITY
       (224) .. (604)
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                                                       ISOFORMS WITHOUT EXONS 6 TO
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Best Local Similarity 66.3%;
Matches 492; Conservative
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LOCATION: (507)...\556;
OTHER INFORMATION: MISSING (
NAME/KEY: VARSPLIC
LOCATION: (536)..(536)
OTHER INFORMATION: N -> R (?
NAME/KEY: VARSPLIC
NAME/KEY: VARSPLIC
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LOCATION: (46)..(46)
OTHER INFORMATION: R -> P (IN IN(A) ANTIGEN)
-09-983-000A-16
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NAME/KEY: VARSPLIC
LOCATION: (266)...(273)
OTHER INFORMATION: MISSING (
OTHER INFORMATION: M 7)
NAME/KEY: VARSPLIC
LOCATION: (385)...(385)
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LOCATION:
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OTHER INFORMATION: Q ->
NAME/KEY: VARSPLIC
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                    LQPTANPNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDV 291
                                                                                                                                                                           EDFISSTISTTPRAFDHTKQNQDWTQWNPSHSNPEVLLQTTTRMTDVDRNGTTAYEGNWN 360
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Pred. No. 3.3e-188;
1; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-116-275-206
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US-10-116-275-206
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Best Local S
Matches 491
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SOFTWARE: PatentIn version
SEQ ID NO 206
LENGTH: 742
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Publication No. US20030211476A1

GENERAL INFORMATION:

APPLICANT: Elan pharmaceutical Technology
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APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and I
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell R
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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 PEAHPPLIHHEHHEEEETPHSTSTIQATPSSTTEETATQKEQWFGNRWHEGYRQTPKEDS
                                                          EDFISSTISTTFRAFDHTKQNQDWTQWNPSHSNPEVLLQTTTRMTDVDRNGTTAYEGNWN
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Brayden, David
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CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 73
LENGTH: 365
TYPE: PRT
ORGANISM: Mus musculus
US-09-870-759-73
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US-09-870-759-73
Sequence 73, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 870759
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US-09-751-708A-73
IS-09-751-708A-73
Sequence 73, Application US/09751708A
Publication No. US20030157113A1
PUBLICANT TERMAN, David S
PITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
CURRENT PEPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR PEPLICATION NU
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US-10-291-634-3

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CURRENT APPLICATION NUMBER: US/10/291,634
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/288,230
PRIOR FILING DATE: 199-04-08
PRIOR FILING DATE: 199-04-08
PRIOR FILING DATE: 199-07-15
PRIOR APPLICATION NUMBER: 60/021,762
PRIOR APPLICATION NUMBER: 60/021,762
PRIOR FILING DATE: 1996-07-15
VIMMER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 339
TYPE: PRI
ORGANISM: Rattus sp.
RESULT 7
US-10-156-932-18
; Sequence 18, Application US/10156932
; Publication No. US20030069181A1
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Publication No. US20030105058A1
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Best Local
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APPLICANT: Gentz, Reiner L
APPLICANT: Dillon, Patrick J
TITLE OF INVENTION: CD-44 Like Protein
FILE REFERENCE: 1488.0490003
                                                                                                                                                        477
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                                                                                                                 TADETRNIQNVDMKI 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NPNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDKVWWHTAWGLLCLLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFN
                                                                                                                                                                                                              VCIAVNSRRRCGQKKKLVINSGNGAVEDRKÞSGINGEASKSQEMVHLVNKESSETPDQFM 476
                                                                                                                                                                                                                                                                                                 QDTFHPSGGSHTTHGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILA 416
                                                                                                                                                                                                                                                                                                                                                                      DPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVSSGSTIEK-STPEGYILHT------DLP------TSQPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVSSGSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLOPTA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCTNASAPLEEDCTSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCFNASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTLPTMAQMELALRKGFETCRYGFIEGHVVIPRIHPNAICAANNTGVYILLASNTSHYDT 120
                                                                                                                                                                                         VCIAVNSRRRCGQKKKLVINSGNGTVEDRKPSELNGEASKSQEMVHLVNKEPTETPDQFM 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.8%; Score 1299; DB 14; Ilarity 56.4%; Pred. No. 2.3e-95; Conservative 18; Mismatches 38;
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GENERAL INFORMATION:

APPLICANT: Wong, Albert J.

TITLE OF INVENTION: Alternative Splice Forms of Proteins as ITILE OF INVENTION: Basis for Multiple Therapeutic Modalities FILE REFERENCE: 8321-81

CURRENT APPLICATION NUMBER: US/10/156,932

CURRENT FILING DATE: 2002-05-28

PRIOR APPLICATION NUMBER: US 60/293,791

PRIOR APPLICATION NUMBER: US 60/293,791

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOTE: 82

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 143

TYPE: PRT

GRANISM: Homo Sapiens

US-10-156-932-18
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; ORGANISM: Homo Sapiens
US-10-156-932-20
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US-10-156-932-20
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TITLE OF INVENTION: Alternative Splice Forms of Proteins as
TITLE OF INVENTION: Basis for Multiple Therapeutic Modalities
FILE REFERENCE: 8321-81
CURRENT PILLIG BATE: 2002-05-28
CURRENT FILING BATE: 2002-05-28
PRIOR APPLICATION NUMBER: US 60/293,791
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 186
LEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application No. US20 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 185
   344
                                                                          110
                                                                                                                                          284
                                                                                                                                                                                                                                                       224 MDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                           176 DDVSSGSSSERSSTSGGYIFYTFSTVHPIPDEDS-----PWITDSTDRIPATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VTAVTVGDSNSNVNRSLSGDQDT 143
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                                                                                                                                                                                                                                                                                                                                                        1 DRIPATSTSSNTISAGWE------PNEESEDERDRHLSFSGSGIDDDEDFISSTN
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   DSNSNVNRSLSGDQDT 359
                                                                                                                                                                                                                 MDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTL
                                                                                                                                      TSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVG
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                                                                          TSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVG
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76.0%;
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DSNSNVNRSLSGDQDT

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GENERAL INFORMATION:

APPLICANT: Wong, Albert J.

APPLICANT: Wong, Albert J.

TITLE OF INVENTION: Basis for Multiple Therapeutic Modalities

FILE REFERENCE: 8321-81

CURRENT APPLICATION NUMBER: US/10/156,932

CURRENT FILING DATE: 2002-05-28

PRIOR APPLICATION NUMBER: US 60/293,791

PRIOR APPLICATION NUMBER: US 60/293,791

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

SEQ ID NO 22

LENCTH: 187
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US-10-156-932-22
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; ORGANISM: Homo Sapiens
US-10-156-932-16
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Publication No. US20030069181A1

GENERAL INFORMATION:

APPLICANT: Wong, Albert J.

TITLE OF INVENTION: Alternative Splice Forms of Proteins as

TITLE OF INVENTION: Basis for Multiple Therapeutic Modalities

FILE REFERENCE: 8321-81

CURRENT APPLICATION NUMBER: US/10/156,932

CURRENT FILING DATE: 2002-05-28

DEPTOR ADSTRUCTURE TO THE TOWN THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              Matches 103;
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/293,791
PRIOR FILING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131
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                                              316 PHTKESRTFIFVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDT 359
                                                                                                                                                                                                             256 TQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHY 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSHPMQGRTTPSPEDSSW-TDFFNPISHPMGRGHQAGRRMDMDSSHSTTLQPTANPNTGL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQDT 187
                                                                                                                                                           TKQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEDIDRIGPISMITQQSNSQSFSTSHEGLEEDKDHFITSTLISSNRNDVIGGRRDPNHSE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10156932
Vo. US20030069181A1
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                                                                                                                                                                                                                                                                                                                                                    20.6%;
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82.5%;
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                                                                                                                                                                                                                                                                                                          Score 537; DB 14; Length 109; Pred. No. 2.9e-35; 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 718; DB 14; Length 187; Pred. No. 2.2e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels 18;
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Sequence 8, Application US/09927463
publication No. US20030032621A1
GENERAL INFORMATION:
APPLICANT: I.N.S.E.R.M.

TITLE OF INVENTION: Means for regulating hematopoietic differentiation FILE REFERENCE: 1113
CURRENT APPLICATION NUMBER: US/09/927,463
CURRENT FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1

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                                                                                                                                                                                                                                                                                                                                                                              NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEE26
TELECOMMUNICATION INFORMATION:
TELEPANE: 212-628-5197
TELEPAX: 212-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                          Matches
                                                                                                                                                          Local Similarity
les 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-WAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, V CURRENT APPLICATION DATA: US/09/799,118 APPLICATION NUMBER: US/09/799,118 FILING DATE: 06-Mar-2001 CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                            92 HPNSICAANNTGVYILTSNTSQYDTYCFNA 121
                                                                                                                   32 GVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFETCRYGFIEGHVVIPRI 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09799118
                                                                            GVPHVEKNGRYSISRTEAADICKAFNSTLPTMAQMEKALSIGFETCRYGFIEGHVVIPRI
                                                                                                                                                                                                                                                                                                                     LENGTH: 90 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
HPNSICAANNIGVYILISNISQYDIYCFNA 90
                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wisniewski, Hans Georg
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                                                                                                                                                                            18.3%;
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Therefor and Uses Thereof
                                                                                                                                                          1; Mismatches
                                                                                                                                                                              Score 478; DB 9;
Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEE26/VILCEK=1B
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                                                                                                                                                             0
                                                                                                                                                                                                    Length 90;
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                                                                                                                                                               Indels
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                                                                                                                                                               Gaps
                                                                                  60
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GENERAL INFORMATION:

APPLICANT: Wong, Albert J.

TITLE OF INVENTION: Alternative Splice Forms of Proteins as

TITLE OF INVENTION: Basis for Multiple Therapeutic Modalities

FILE REFERENCE: 8321-81

CURRENT APPLICATION NUMBER: US/10/156,932

CURRENT FILING DATE: 2002-05-28

PRIOR APPLICATION NUMBER: US 60/293,791

PRIOR APPLICATION NUMBER: US 60/293,791

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 82

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 79

TYPE: DET
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US-10-156-932-14
; Sequence 14, App
; Publication No.
                                                                                                                                                                                                                                                            RESULT 14
US-10-052-641-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Homo Sapiens
US-10-156-932-14
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                       SEQ ID NO 8
                                                                                                                                                                                                                             Sequence 2, Application US/10052641 Publication No. US20030032073A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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SEQ ID NO 2
LENGTH: 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 18.1%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                343
                                                                                                                                                                                                                                                                                                                                                                                                      283 LISSNRNDVIGGRRDPNHSEGSTILLEGYTSHYPHIKESRIFIPVISAKIGSFGVTAVIV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 ICLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALS
                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                GDSNSNVNRSLSGDQDT 359
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No. US20030069181A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 386; DB 14; Length 79; Pred. No. 2e-23; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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; TYPE: PRT
; ORGANISM: Homo
US-10-052-641-2
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                            CURRENT FILING DATE: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PRILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21990
PRIOR APPLICATION NUMBER: PCT/US99/21990
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
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Patent No.
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Best Local
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 RNDVTGGRRDPNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNS
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. US20020132240A1
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57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Cao, Wei-Qiang
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoni, Nicholas F.
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Filvaroff, Ellen
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art, Timothy A.
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A.
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PCT/US99/28313
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Pred. No. 1.4e-20;
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PRIOR FILLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/3095
PRIOR APPLICATION NUMBER: PCT/US99/3095
PRIOR APPLICATION NUMBER: PCT/US99/3095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
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Search completed: March 8, 2004, 06:22:12 Job time: 398 secs
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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3: /cgm2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgm2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

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GENERAL INFORMATION:

    Application US/07946497
    5506119
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Result

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## ALIGNMENTS

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COUNTEX: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
CLASSIFICATION NUMBER: 29,768
APPLICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELETAX: (202)672-5390
TELETAX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: hCD44

***COUNE: hCD44
Query Match 70.1%;
Best Local Similarity 72.6%;
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: GUENTHERT, Ursula
APPLICANT: MATZGU, Siegfried
APPLICANT: MATZGU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
CITY: Washington, D.C.
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RY: USA
  Score 1827; DB 1; Length 361; Pred. No. 3.6e-156; O; Mismatches 3; Indels 13:
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       Indels 132;
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RESULT 2
US-08-483-322-6
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   ZIP: 20007-5109
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/483,322
FILING DATE: 07-7UN-1995
CLASSIFICATION DATA:
APPLICATION UNMBER: US 07/946,497
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: HERRLI
APPLICANT: PONTA,
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C. COUNTRY: USA
REFERENCE/DOCKET NUMBER:
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MATZKU, Siegfried
WENZL, Achim
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16915/145
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; Patent No. 5885575
; GENERAL INFORMATION
; APPLICANT: HERRLICI
; APPLICANT: PONTA, 1
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US-08-478-882-6
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Best Local Similarity 72.6
Matches 358; Conservative
                                                          APPLICANT: GUENTHERT, Ursula
APPLICANT: MATZKU, Slegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS.
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
            ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
 COUNTRY:
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o. 5885575
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Suite 500

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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: hCD44
US-08-483-322-6
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TELEPAX: (202)672-5399
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TRNLQNVDMKIGV 361
                            TRNLQNVDMKIGV 493
                                                                                                                      VNSRRRCGOKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE
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                                                                                 VNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE
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Pred. No. 3.6e-156;
0; Mismatches 3;
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,882
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,497
APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPAX: (202)672-5309
TELEFAX: (202)672-5399
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CLONE: hCD44
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                     TRNLQNVDMKIGV
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                                                                    VNSRRRCGOKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADE
TRNLQNVDMKIGV 361
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RESULT 5
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FILING DATE: 12-DEC-1990
APPLICATION NUMBER: 325,224
FILING DATE: 17-MAR-1989
SEQ ID NO:2:
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; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/C
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
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APPLICANT: ST.JOHN, THOMAS P.;GALLATIN,
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Best Local Similarity 68.2
Matches 337; Conservative
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                                                                                     ETRNLQNVDMKIGV 493
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                                                                 ETRNLONVDMKIGV 362
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Sequence 2, Application US/07946497

Patent No. 5506119

GENERAL INFORMATION:
APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: MATZKU, Stegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION MUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: MINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
COUNTRY: USA
7TP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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                                                                                                                                                                                                                                                                                                                          240 RTQWNPIHSNPEVILQTTTR-----MTDIDRNSTSAHGENWTQBPQPPFNNHEYQDEEET 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 DVSSGSSSERSSTSGGYIFYT-FSTVHPIPDED------SPWITDST----D 217
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447
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                                                                                                                                                                                                                                           295 PHATSTTWADPNSTTEEAATQKEKWFENEWQGKNPPTPSEDS-HVTEGTTASAHNNHPSQ 353
                                                                                                                                                                                                                                                                                  276 DHPTTSTLTSSNRNDVTG------GRRDPNHSEGSTTLLEGYT--SHYPHTKE 320
                                                                                                                                                                                                                                                                                                                                                                    218 RIPATNMDSSHSTTLOPTANPNTGLVEDLDR--TGPLSMTTQQSNSQSFSTSHEGLEEDK 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TILPTMAQMELALRKGFETCRYGFIEGHVVIPRIHPNAICAANNTGVYILLASNTSHYDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STLPTWAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYI-LTSNTSQYDT 116
                                                                            HSHGSQEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIAVNSRRRCGQXKKLVIN 436
                                                                                                                                                                                                                                                                                                                                                                                                         DVSSGSTIEK-STPEGYILHTDLPTSQPTGDRDDAFFIGSTLATIATTPWVSAHTKQNQE
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                     SGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFMTADETRNLQNVDMKIGV 493
SGNGTVEDRKPSELNGEASKSQEMVHLVNKEPTETPDQFMTADETRNLQSVDMKIGV 503
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RESULT 6

Q	B &	S & 8	D 99	g Qy	dg VQ	Query Best : Match	Sequence of Sequen	
276 DHPTTSTLTSSNRNDVTG		- DVSSGSTIEK-STPEGYILHTDLFTSQFTGDR	YCENASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDD	58 STLPTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYI-LTSNTSQYDT 116 	1 MDKFWMHAAWG-LCLVPLSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADI                :	ry Match 54.6%; Score 1425; DB 1; Length 503; t Local Similarity 58.7%; Pred. No. 9.6e-120; ches 315; Conservative 36; Mismatches 108; Indels 78; Gaps 16;	equence 2, Application US/08483122  atent No. 5760178  BREAL INFORMATION: APPLICANT: HERRIICH, Peter APPLICANT: HERRIICH, Peter APPLICANT: HONTA, Helmut APPLICANT: GUNNTHERT, Ursula APPLICANT: HERRIICH, Seigfried APPLICANT: HERRIICH, Seigfried APPLICANT: HERRIICH, Seigfried APPLICANT: HERRIICH, SAINT CD44 SURFACE PROTEINS, DNA TITLE OF INVENTION: AS WELL AS THER USE IN DIAGNOSIS AND THERAPY NUMBER OF SEQUENCES: 8  CORRESPONDENCE ADDRESS: ADDRESSE: FOLSY & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: WEARING, D.C. COUNTRY: USA COMPUTER READING FORM: MEDIUM TYEE: Flopy disk COMPUTER READING PO-DOS/MS-DOS SOFTWARE: PATENTION DATA: APPLICATION NUMBER: US06/463,322 FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION APPLICATION NUMBER: US07/946,497 FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION APPLICATION NUMBER: 129.768 REFERENCE/DOCKST NUMBER: 16915/145 TELECOMMUNICATION DATA: REGISTRATION UNDERS: 12021672-5309 TELEPAN: (202)672-5399 TELEPAN: 1003 amino acids TYDE: amino acids TYDE: amino acids TYDE: amino acids TYDE: amino acids TYDE: protein 08-483-322-2	1 3 3

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Sequence 2, Application
patent No. 5885575
GENERAL INFORMATION:
APPLICANT: HERRIIC
APPLICANT: PONTA,
APPLICANT: PONTA,
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US-08-478-882-2
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US-08-478-882-2
                                                                                                                            Query Match
Best Local S
Matches 315
                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946
FILING DATE: 19921109
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1691
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GUENTHERT, Ursula
APPLICANT: MATZZU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
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                                                                                                                              Similarity 58.7
15; Conservative
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STLPIMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYI-LTSNTSQYDT
                                                                            MDKFWWHAAWG-LCLVPLSLA--QIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFN 57
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                                                      MDKVWMHTAWGLLCLLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFN
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GUENTHERT, Ursula
MATZKU, Siegfried
WENZL, Achim
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3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                 : (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HERRLICH, Peter
                                                                                                                                                                                                                      protein
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                                                                                                                            ; Score 1425; DB 2;
; Pred. No. 9.6e-120;
36; Mismatches 108;
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                                                                                                                                                                  Length 503;
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Patent No.
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1691
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
   SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acid
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                  TELEFAX: 12.
TELEFAX: 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSHGSQEGGANTTSGPIRTPQIPEWLIILASILALALILAVCIAVNSRRRCGQXXXLVIN 436
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                         : 363 amino acids AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUENTHERT, Ursula
MATZKU, Siegfried
WENZL, Achim
WENZL, Achim
VENTION: VARIANT CD44 SURFACE PROTEINS, DNA
VENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS
VENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
                                                                                                                   (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PONTA, Helmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HERRLICH, Peter
                                                                              7:
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US-08-483-322-7
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                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08483322
Patent No. 5780178
GENERAL INFORMATION:
APPLICANT: HERRLICH, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 288; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,322
FILING DATE: 07-JUN-1995
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CLONE: mCD44
                                                                                                                                                                                     APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: GUENTHERT, Ursula
APPLICANT: MATZKU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                              COUNTRY:
                                                                                                                                            ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W CITY: Washington, D.C.
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57.9%; pred
twe 28;
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Pred. No. 7.6e-114;
28; Mismatches 43;
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                                                 Version
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US-08-478-882-7
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Patent No. 5885575
GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION UNMERS: US 07/946
PILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1691
TELECHMONICATION INFORMATION:
TELEPHONE: (202)672-5309
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acid
TYPE: amino acid
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                                                 APPLICANT:
APPLICANT:
         APPLICANT: MATZKU, APPLICANT: WENZL, I
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                       GUENTHERT, Ursula
MATZKU, Siegfried
WENZL, Achim
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                                                                     PONTA,
                                                                              HERRLICH,
                                                                  Helmut
            VARIANT CD44
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            SURFACE
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59 TLPTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVVIL-TSNTSQYDTY
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                                                      VCIAVNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFM
                                                                                                                    ----GSSRTVTHGSELAGHSSANODSGVTTTSGPMRRPQIPEWLIILASLLALALILA
                                                                                                                                                                    DTFHPSGGSHT-THGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILABLLALALILA 416
                                                                                                                                                                                                                                                                                  PNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQ
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VCIAVNSRRRCGQKKKLVINGGNGTVEDRKÞSELNGEASKSQEMVHLVNKEPSETFDQCM 346
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                                                                                                                                                                                                                                              Length 363;
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177 120 117 60 58

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476 286 297

208

Gaps

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DNA

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US-08-478-882-7
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/946
PILING DATE: 19921109
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1691
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: mCD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                              PNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRD 297
                                                                                                                                                                                                                                                                                                                                        VSSGSSSERSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPATNMDSSHSTTLQPTAN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLPTMDQMKLALSKGFETCRYGFIEGNVVIPRIHPNAICAANHTGVYILVTSNTSHYDTY
                          VCIAVNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNKESSETPDQFM
                                                                                                        DTFHPSGGSHT-THGSESDGHSHGSQEGGANTTSGPIRTPQIPEWLIILASILLALILIA 416
                                                                                                                                                                                     PNHSEGSTTLLEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGDQ 357
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VCIAVNSRRRCGQKKKLVINGGNGTVEDRKPSELNGEASKSQEMVHLVNKEPSETPDQCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 1357; DB 2;
; Pred. No. 7.6e-114;
28; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16915/145
                                                                                                                                                -SKDSR-----------
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
COMPUTER READABLE FLORY disk
MEDIUM TYPE: Flory disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/021,762
FILLING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                    237 NPNTGLVEDLDRTGPLSMTTQQSNSQSFSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRR
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                                                                                                                                                                                                                                      58 STLPTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYI-LTSNTSQYDT 116
                                                                                                                                                                                                                                                                                   1 MDKVWWHTAWGLLCLLQLSLAQQQIDLNITCRYAGVFHVEKNGRYSISRTEAADLCEAFN
                                                                                                                                                                                                                                                                                                           MDKFWWHAAWG-LCLVPLSLA--QIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFN
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                                                                                                                                  YCFNASAPLEEDCTSVTDLPNSFDGPVTITIVNRDGTRYSKKGEYRTHQEDIDASNIIDE
                                                                                                                                                        YCFNASAPPEEDCTSVTDLPNAFDGPITITIVNRDGTRYVQKGEYRTNPEDIYPSNPTDD 176
                                                         DVSSGSTIEK-STPEGYILHT-----
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DILLON, PATRICK J.
VENTION: CD44-LIKE PROTEIN
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linear
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US-07-946-497-4
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                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 354 amino acid
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
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                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                            Local Similarity
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                                                                     YRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYIFYTFSTVHPI-----PDEDSPWITD 214
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                                      YRQTPRE-----DSHSTTGTAAASAHTS-----HPMQGRTTPSPEDSSW-TD
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3000 K Street, N.W., Suite 500
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                                                                                                           Conservative
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SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
                                                                                                         27.3%; Score 711; DB 1; Length 354; 70.0%; Pred. No. 1.1e-55; tive 10; Mismatches 18; Indels
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 ATMMDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTTQQSNSQS 263
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                                                                                                           36;
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                                                                                                                                                                                Best Local Similarity Matches 149; Conserv
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/483,322
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,497
PILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 354 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
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     FSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHYPHTKESRT 323
                                                                                                                                             YRTNPEDIYPSNPTDDDVSSGSSSERSSTSGGYIFYTFSTVHFI-----PDEDSPWITD
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                                        FFNPISHPMGRGHQAGRRMDMDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTTQQSNSQS
                                                                            STDRIP---
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GUENTHERT, Ursula
MATZKU, Siegfried
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                                                                                                                                                                                                                                                                                                                              354 amino acids
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WENZL, Achim
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                                                                                                                                                                                    Conservative
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                                                               ---ATNMDSSHSTTLOPTANPNTGLVEDLDRTGPLSMTTQQSNSQS
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US-08-478-882-4
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Best Local Similarity 70.0
Matches 149; Conservative
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GENERAL IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946
FILING DATE: 19921109
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1691
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MATZKU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
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CITY: Washing
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 354 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
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                                                                                                                                                   215 STDRIP-----ATMMDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTTQQSNSQS 263
                                                                                                                                                                                                                             161 YRTNEBDIYESNETDDDVSSGSSSERSSTSGGYIFYTFSTVHPI-----PDEDSPWITD
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FIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGD 356
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                                    FSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHYPHTKESRT 321
                                                                         FSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHYPHTKESRT
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GUENTHERT, Ursula
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                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                              27.3%; Score 711; DB 2; Length 354; 70.0%; Pred. No. 1.1e-55; tive 10; Mismatches 18; Indels
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RESULT 15
US-08-359-850-2
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Best Local S
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APPLICANT: Z ller, Margot
APPLICANT: Herriich, Peter
APPLICANT: Herriich, Peter
APPLICANT: Herriich, Peter
APPLICANT: Herriich, Helmut
TITLE OF INVENTION: for Immunosuppression
TITLE OF INVENTION: for Immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMGTH: 338 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/359,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-ULITERION:
FILING DATE: 23-ULITERION:
TELECOMMUNICATION INFORMATION:
TOTREPHONE: (202) 833-7533
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APPLICATION NUMBER:
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nes 147; Conservative
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CLASSIFICATION:
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308
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                                                                                              FSTSHEGLEEDKDHPTTSTLTSSNRNDVTGGRRDPNHSEGSTTLLEGYTSHYPHTKESRT
                                                                                                                                     FFNPISHPMGRGHQAGRRMDMDSSHSTTLQPTANPNTGLVEDLDRTGPLSMTTQQSNSQS
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 FIPVTSAKTGSFGVTAVTVGDSNSNVNRSLS
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Search completed: March Job time : 26 secs

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